POPULATION GENETIC STRUCTURE OF *CONOPHTHORUS PONDEROSAE* HOPKINS (COLEOPTERA: SCOLYTIDAE) INFERRED FROM MITOCHONDRIAL DNA HAPLOTYPES

A Thesis

by

KATRINA LOUISE MENARD

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE

August 2006

Major Subject: Entomology

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Approved by:

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ABSTRACT

Population Genetic Structure of *Conophthorus ponderosae* Hopkins (Coleoptera: Scolytidae) Inferred from Mitochondrial DNA Haplotypes. (August 2006)

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Pine cone beetles (*Conophthorus* sp.*)* are serious pests of many forest ecosystems since they burrow into pine cone tissues for egg deposition, causing the death of the seeds. Management of these beetles in natural and commercial stands of pines has been problematic due to lack of understanding about species limits and distribution. This study was conducted to investigate the phylogeography and phylogenetics of the genus. Several species represented by disjunct populations appear to be monophyletic including *Conophthorus edulis*, *C. mexicanus, C. coniperda*, and *C. conicollens,* whereas *C. ponderosae* is polyphyletic with many distinct clades isolated by geography. This study explored whether host use or geography has played a greater role in the diversification of this genus, focusing on the polyphyletic *C. ponderosae* and the monophyletic *C. edulis*. In the first study, 751bp of the mtDNA CO1 gene were sequenced to reconstruct a phylogeny of the genus, and the distribution and host use were compared to investigate whether these factors were significantly associated. The second study addressed population structure and possible historical influences on the *C. edulis* and *C. ponderosae* populations using a nested clade analysis of the mtDNA haplotypes. Despite potential limitations due to sampling, several conclusions could be drawn. Three separate haplotype networks were found for the *C. ponderosae* haplotypes, indicating that there

have been at least three lineages that have associated with *P. ponderosa*. Geography was significantly associated with the phylogeny at greater distances (>900km), but host use was not significant. At the species level, association with geography is variable. Population structure for *C. ponderosae* at the species level is minimal, and suggests that there has not been much time for lineage sorting of the haplotypes based on the nested clade analysis as compared to *C. edulis*.

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CHAPTER I
INTRODUCTION

Interactions between plants and insects have undeniably influenced the diversification of both kingdoms, with both macro- and microevolution influencing lineage diversification (Feder et al. 1988, Funk 1998, Roininen et al. 1993, Mopper 1996). Herbivory incurs unavoidable selection pressures because plant secondary chemical compounds are often toxic. Insects that feed internally in plant tissues experience a potentially more toxic environment as compared to external feeders because they are surrounded by secondary chemicals (Mopper 1996). Thus, selection for toxin resistance would likely evolve in a lineage of herbivores consistently feeding in a particular host species (Edmunds and Alstad 1978). Once toxin resistance for a particular plant becomes established for a herbivore population, increased efficiency outweighs the genetic (Scheirs et al. 2005) and physiological costs of feeding on alternate hosts (Fox and Morrow 1981). Isolation of populations and lineage diversification would likely ensue as a result (Roinenen et al. 1993, Funk 1998).

This evolutionary scenario may, in part, explain the diversification of the ponderosa pine (*Pinus ponderosa* Laws) cone feeding scolytid, *Conophthorus ponderosae* Hopkins. These beetles lay eggs and rear offspring inside second-year cones, and they are often completely bathed in pine resin as they burrow inside the cone (Hopkins 1915, Schaefer 1962, Kinzer et al. 1970). Pine secondary-chemical compounds mostly consist of monoterpenes, which exhibit varied levels of toxicity (Philips and Croteau 1999, Edmunds and Alstad 1978). The combination of these chemicals and their

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This thesis follows the style of *Molecular Ecology*.

concentration varies among species and populations (Philips and Croteau 1999, Conkle and Critchfield 1988). Thus, beetle populations are exposed to variety of monoterpene toxins depending on what stands of trees they attack. *Conophthorus ponderosae* occurs throughout western Canada, the U.S.A and Mexico, and has the widest host breadth of all the species of *Conophthorus* (Wood and Bright 1992). *Pinus ponderosa* is the main host of this beetle, and occurs throughout the beetle's range (Critchfield and Little 1966). It is divided into four subspecies (*P. ponderosa benthamiama, P. ponderosa ponderosa, P. ponderosa scopulorum*, and *P. ponderosa brachyptera*), and each exhibits a unique complex of monoterpenes (Conkle and Critchfield 1988). Variation in host sub-species use has been shown to be significant in at least one species of scolydid that feeds on *P. ponderosa* (Kelley et al. 1999). *Conophthorus ponderosae* lineages potentially diversified in association with these hosts given the variation in monoterpenes among *P. ponderosa* populations.

Diversification of other scolytids in association with host use has been observed with some species (Kelley et al. 1999, Kerdelhue´ et al. 2002, Jordal et al. 2002). However, lineage diversification among other species, including *Conophthorus* spp., has shown little association with host (Cognato et al. 2003, Cognato et al. 2005, Kelley and Farrell 2005, Stauffer et al. 1999). Cognato et al. (2005) investigated the species limits of *Conophthorus* and the association of host use and geography with lineage diversification. Phylogenetic analysis revealed that most species were monophyletic, except *C. ponderosae,* whose individuals were distributed among three unrelated clades. These patterns of lineage diversification were best explained by association with geographic distribution, with lineages separated by distances greater than 200-300 km. Lineages

were not associated with host use, except within the Western United States. In this exception, lineages of *C. ponderosae* were associated with taxonomic sub-sections of *Pinus*. Hence, *Conophthorus* lineages were related mostly by geographic proximity. However, host influence on lineage diversification may occur locally (Mopper 1996). The extent of local association with host throughout the range *C. ponderosae* could not be assessed because of limited samples (Cognato et al. 2005).

The dynamic landscape and environment of the Pleistocene era (~2 million – 10,000 years before present) had a significant effect on the flora and fauna of the southwestern United States. During this time multiple glaciations in North America caused different climatic cycles, which frequently redistributed ecosystems (Webb and Bartlien 1992). During the colder periods, which lasted approximately 100,000 years, present-day pine forest ecosystems were general distributed in more southern latitudes (Webb and Bartlein 1992). These systems generally moved northward during warmer interglacial periods, which lasted approximately 10,000 years (Prentice et al. 1991). During the colder period the dominant habitat, pinyon- juniper (*Pinus edulis* and *Juniperus scoluprum*), was likely present in its current distribution but at lower altitudes (Van Derender 1986, Holmgren et al. 2003, Bentacourt et al. 1991). Other forest habitats, such as ponderosa pine (*Pinus ponderosa* Law) did not exist beyond the northern border of New Mexico (Conkle and Critchfield 1988, Axelrod 1986, Spaulding 1990, Van Devender 1986). These pine habitats only recently reached their most northern and attitudely high distributions after the recession of the last major ice-sheet, approximately 10,000 bp (Bentancourt et al. 1991,Walter and Epperson 2001, Conkle and Critchfield 1988). The contraction and retraction of habitats often isolated populations (Betancourt et

al. 1991, Smith and Farrell 2005). This isolation left a footprint on the evolution of these species. For example, multiple genetic loci of pine species present in the North-West indicate that there was isolation between ponderosa pine populations east and west of the Rocky Mountains during the Pleistocene. Moreover, other populations were isolated, as suggested by morphological and chemical differences found among *P. ponderosa* subspecies (Conkle and Critchfield 1988).

Differential spatial and temporal histories of the pine species in the southwest influenced the distribution and genetic history of many associated organisms (Kelley et al. 1999, Wilson et al. 2005). Insects that feed on southwestern pines, specifically bark beetles (Scolytinae) should share a closer historical association. For example, an isolation event in Mexico and in association with *P. cembroides* likely contributed to the divergence of the sister species, *Ips hoppingi* and *I. confusus* (Cognato et al. 2003). However, *I. confusus* remained monophyletic despite several isolation events of beetle and host trees (*P. edulis* and *P. monophylla*) (Cognato et al. 2003). In the case of species of *Dendroctonus* beetles that feed on southwestern pines, such as *P. ponderosa* or *P. flexilis*, are closely related (Kelley and Farrell 2005) and some species exhibit genetic subdivision among populations associated with different hosts (Kelley et al. 1999).

This study explored whether host use or geography has played a greater role in the diversification of this genus, focusing on the polyphyletic *C.ponderosae* and the monophyletic *C. edulis*. In the first study, 751bp of the mtDNA CO1 gene were sequenced to reconstruct a phylogeny of the genus, and the distribution and host use were compared to investigate whether these factors were significantly associated. The second

study addresses population structure and possible historical influences on the *C. edulis* and *C. ponderosae* populations using a nested clade analysis of the mtDNA haplotypes.

CHAPTER II

HOST USE AND GEOGRAPHY

Introduction

This study examined multiple individuals from different pine species, including *P. ponderosa* subspecies from Mexico, the southwestern United States, the Rocky Mountains and the northwestern United States. By augmenting the data set in this fashion and using the analytical methods of Cognato et al. (2005), I tested for an association among *C. ponderosae* lineages and host. I hypothesize that local lineage diversification does not associate with host use. Alternatively, lineage diversification associates with geographic proximity.

Materials and Methods

Specimens and molecular protocols

One to 10 individuals were sampled from locations in United States and Mexico, and collections included *C. ponderosae* and related species. For *C. ponderosae*, 152 individuals from 21 different populations were examined (Table 2.1 in Appendix A, Appendix C).

Live specimens were excised, using a knife and forceps, from infested cones and preserved in 100% ethanol until molecular analysis. Individuals from each locality were collected from different pine cones to prevent repeat sampling of the same brood. Tissue was extracted from the pronotum of the beetle, and the remaining body parts were

mounted and vouchered at Texas A&M University, Department of Entomology Insect Collection. Each mounted specimen was given an individual number, ranging from 160-454 based on its extraction order to associate it with its genomic sequence. Total genomic DNA was extracted using a silica-based spin column procedure following the manufacturer's protocol (i.e.Qiamp, Qiagen Inc., Santa Clara, California).

A section of approximately 823 nucleotides of the mtDNA COI gene was amplified using the polymerase chain reaction (PCR) with primers "Jerry" (5' CAACATTTATTTTGATTTTTTGG 3'; location 2183 within the *Drosophila yukuba* COI) and "Pat" (5 ATCCATTACATATAATCTGCCATA 3'; location 3014 in tRNA region flanking COI). Each reaction contained 35µL ddH_20, 5µL 10 X *Taq* DNA polymerase buffer (Promega Corporation, Madison, Wisconsin), 4µL 25mM Promega $MgCl_2$, 1µL 40mM deoxynucleotide triphosphates (dNTPs), 2µL of each 5mM oligonucleotide primer, 0.5µL of Promega *Taq* DNA polymerase and 1.5µL of DNA template. The PCR was performed on a thermocycler (MJ Research, Boston, Massachusetts) under the following conditions: one cycle for 2 min. at 95ºC, 35 cycles of 1 min. at 95ºC, 0.75 min. at 55ºC, 1 min. at 72ºC, and a final elongation cycle of 5 min. at 72ºC.

Unincorporated oligonucleotides and dNTPs were removed from the PCR products using the Qiaquick PCR purification Kit (Qiagen Inc.) and were directly sequenced on an ABI 377 automated sequencer following a Big Dye (Applied Biosystems, Inc., Foster City, California) florescent chemistry reaction. Both sense and antisense strands were sequenced for all individuals.

Sequence analysis

Sequencher™, 4.1 or 4.2 (Gene Codes Corporation, Ann Arbor, Michigan) was used to edit both strands of DNA, which yielded an edited sequence of 751bp s for 253 individuals. Sequence alignment was unambiguous because of complete amino acid conservation and the absence of insertion or deletion events. PAUP* 4.0 (Swofford, 1998) was used to estimate the phylogenetic relationships of the species of *Conophthorus.* Unique haplotypes from each population were isolated for phylogenetic analysis. A heuristic search using the simple search parameter and 1000 replicates using TBR branch swapping was used to reconstruct phylogeny. A bootstrap analysis was also used to estimate support of the branches within the clades with a heuristic search with fast stepwise addition and 1000 replicates, followed by TBR branch swapping.

Two methods were used to test the association of geography and host use to the phylogeny of *Conophthorus*. For geography, a pairwise distance matrix was constructed using the latitude and longitudinal data of the sampling localities. Distances in kilometers were calculated using a web-based distance calculator (http://www.indo.com/cgi-bin/dist), which corrected for global circumference. The distances were then imported into PAUP* 4.0 as a NEXUS file, and a distance matrix was constructed. An unweighted pair group method with arithmetic mean (UPGMA) analysis constructed a tree based on the geographical data. Groupings of geographical locations were placed into subsets representing 200-300 km, the approximate distance many bark beetles have been shown to disperse (Jactel and Gaillard, 1991). As per Cognato et al. (2005), populations greater than 900 km were compared as well.

Geographical groupings were then compared to groups of haplotypes based on the phylogenetic trees. These groupings or evolutionarily significant clades (ESCs) were created by counting the branch lengths of the haplotypes. Groups with at least 8 mutational steps to the nearest node (approximating 10% sequence divergence) were considered to be ESCs as in Cognato et al. (2005). Individuals that were determined to be a different species by being incorporated within a clade of individuals from another species (ex: *C. michoacana*) were isolated as their own clade. Hosts were also compared to the ESCs along with geography by grouping the trees according to species, subspecies, and subgenera (see Appendix A).

A Monte Carlo simulation was used to compare the host use (subgenera, species and subspecies) and the two geographical parameters (200-300km, >900km) to the patterns in the phylogeny based on the methodology of Cognato et al. (2005). Only unique haplotypes from each locality were used to compare associations to increase the statistical power. The data were randomized and then compared to see whether there was a significant difference from a random distribution for host use and geographical parameters. Chi-square results that were less than 5% are considered significantly non-random.

Results

Maximum parsimony analysis yielded 1,876 equally parsimonious trees of 744 steps, with a CI of 0.612 and RI of 0.892 (Figure 2.1 in Appendix B). Bootstrap values for all nodes were at least 50%. Due to the number of terminal taxa and the size of the tree, not all of the bootstrap percentages are shown in the figure. As in previous studies,

Conophthorus ponderosae was polyphyletic, with at least three major clades: two that encompass localities from the southwest, and one from the northeast/California. The overall structure of the major lineages did not change from Cognato et al. (2005) (Figures 2.2-2.5).

Phylogenetic patterns of host use and geographic localities were significantly different from patterns of host and localities mapped on random trees. Monte Carlo simulation indicated significant associations of *C. ponderosae* ESCs with geographic areas between 200-300 km and >900 km but there was no association of *C. ponderosae* ESCs with host subgenera or subsections. However, there was a significant association of ESCs and subgenera within areas greater than 900km (Table 2.2).

Discussion

While host use is significant for most of the species of *Conophthorus*, it does not appear significant for *C. ponderosae*. For example, only two of the three clades of *C. ponderosae* were consistently found to feed on the subgenera of *Ponderosae,* while the other clade has a mixture of the subsections *Strobi* and *Ponderosa*e as hosts (Figures 2.6 and 2.7). *C. ponderosae* does not appear to be correlated with the major higher level divisions of pines at the subgenus level (Table 2.2). When considering the biology of *C. ponderosae*, this is not surprising. Females will attack pine cones of other pine species (Furniss 1997), first year cones of *C. ponderosae,* and other tree tissues (Godwin and Odell 1965) given a low abundance of *P. ponderosa* pine cones. If eggs are deposited, larvae often do not survive (Godwin and Odell 1965, Furniss 1997). This suggests that the beetles may opportunistically attack trees rather than being obligate feeders on certain

species. The species is polyphyletic, with at least three major clades sharing a wide breadth of hosts. Despite the lack of a significant association between host use and *C. ponderosae* mtDNA haplotypes, an association was observed with geography. *P. ponderosa* and many of the other western pines are relatively recent migrants to northern North America. Cone beetle species likely had an origin in Mexico, and utilized *P. ponderosa* and other western hosts. They likely followed the movement of their hosts through time. Thus, little time has elapsed for particular *C. ponderosae* lineages to associate with hosts in their Holocene distribution.

Geography does appear to be associated with diversity in *C. ponderosae*, a finding consistent with Cognato et al. (2005). In particular, the grouping of populations that are within more than 900 km of each other had significant results for all members of the genus (Table 2.2). For example, a majority of haplotypes are grouped into geographic areas in the West (Figures 2.6-2.9), with even finer level resolution of some groups to include one clade of mostly populations in the North West and California (Figure 2.6). Within the approximately 200-300km range, groupings also were found to have significant results (Table 2.2). This observation agrees with estimates of dispersal distance (Henson 1962) because individuals do not disperse far from their natal host tree (Schaefer 1962), so distance is a likely barrier for gene flow between populations. The effects of isolation by distance are investigated further in Chapter II. In the case of *C. ponderosae*, while they may have recently arrived in northern North America with their pine hosts, isolation by distance may influence lineage diversification as compared to host choice for the mtDNA haploptyes. More recent adaptations, such as behavioral or local adaptation to hosts within isolated host populations, may not be reflected in

phylogenies using this gene. Future work in other genes such as nuclear or microsatellites may resolve finer levels of adaptive patterns on the local level.

CHAPTER III

POPULATION STRUCTURE

Introduction

Conophthorus is a scolytid beetle whose feeding habits ultimately kills pine cones. Adult behavior of re-infesting natal host trees fosters continual use of a tree and nearby relatives by generations of cone beetle families (Henson 1962, Kinzer et al. 1970). This tight relationship between insect and host could result in isolation of beetle populations that concord with pine migration patterns, and insect speciation in association with specific host use like other host specific insects (Edmunds and Alstad 1976, Mopper 1996). Geographic isolation appears more important in cone beetle lineage diversification, as compare to host use (Cognato et al. 2005 and see Chapter II). However, the historical details of these isolation events are unexplored. In this study, I sample mitochondrial DNA sequences from individuals from multiple localities of a polyphagous pine feeder *C. ponderosae* and monophagous feeder, *C. edulis* and use nested clade analyses to describe historical patterns of *Conophthorus* populations and hypothesize the geographic event that have influenced these patterns (Templeton 1998). Nested clade analysis has been criticized because it lacks an objective means for choosing alternative conclusion of geographic history drawn from the inference key, which is dependent on adequate sampling for accurate results (Knowles and Maddison 2002). Increased sampling efforts focused primarily on the United States and to lesser extent on populations from Mexico. Despite this geographic restriction, nested clade

analysis can still provide insight to possible factors that may have influenced the history of *Conophthorus* lineages.

Materials and Methods

For *C. ponderosae*, 152 individals from 21 populations throughout the southwestern U.S. and Mexico were examined. Nine populations representing 70 individuals were collected for *C. edulis*. One to ten individuals were sampled from each location to gather mtDNA haplotypes for nested clade analysis (Table 3.1 in Appendix A).

Live specimens were excised, using a knife and forceps, from infested cones and preserved in 100% ethanol until molecular analysis. Individuals from each locality were collected from different pine cones to prevent repeat sampling of the same brood. Tissue was extracted from the pronotum of the beetle, and the remaining body parts were mounted and vouchered at Texas A&M University, Department of Entomology Insect Collection. Each mounted specimen was given an individual number, ranging from 160-454 based on its extraction order to associate it with its genomic sequence. Total genomic DNA was extracted using a silica-based spin column procedure following the manufacturer's protocol (i.e.Qiamp, Qiagen Inc., Santa Clara, California).

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polymerase buffer (Promega Corporation, Madison, Wisconsin), 4µL 25mM Promega $MgCl_2$, 1µL 40mM deoxynucleotide triphosphates (dNTPs), 2µL of each 5mM oligonucleotide primer, 0.5µL of Promega *Taq* DNA polymerase and 1.5µL of DNA template. The PCR was performed on a thermocycler (MJ Research, Boston, Massachusetts) under the following conditions: one cycle for 2 min. at 95ºC, 35 cycles of 1 min. at 95ºC, 0.75 min. at 55ºC, 1 min. at 72ºC, and a final elongation cycle of 5 min. at 72ºC.

Unincorporated oligonucleotides and dNTPs were removed from the PCR products using the Qiaquick PCR purification Kit (Qiagen Inc.) and were directly sequenced on an ABI 377 automated sequencer following a Big Dye (Applied Biosystems, Inc., Foster City, California) florescent chemistry reaction. Both sense and antisense strands were sequenced for all individuals

Nested Clade Analysis was performed using the TCS program and statistical parsimony (v.1.13. Clement et al. 2000) to create a haplotype network for *C. ponderosae* and *C. edulis*. Relationships with less than a 95% probability were treated as reticulations. This network was nested as hierarchical groups of haplotypes according to the guidelines outlined by Templeton et al. (1995). GeoDis (v.2.0, Posada et al. 2000) was used to calculate the association between geographical location of haplotypes and the nested haplotype clades. The null hypothesis assumed no association between nested clades and haplotype location. Highly structured populations with limited gene flow were inferred by the rejection of the null hypothesis.

Results

Four haplotype networks were reconstructed using the default settings of TCS for the individuals of *C. ponderosae* and *C. edulis* (Figures 3.1-3.4 in Appendix B). Separate networks were established for each clades separated by more than nine mutational steps. In the case of *C. ponderosae*, three separate networks resulted. The three haplotypes networks created by TCS corresponded to major clades of the *C. ponderosae* phylogeny in Chapter II (Figures 3.1-3.5 in Appendix B), with the northwestern populations being grouped together in one clade (Figure 3.3), and two southwestern clades (Figures 3.2 and 3.4). *C. edulis* had one network (Figure 3.1).

When geography was associated with the haplotype networks using the program GeoDis, only seven of the total 57 clades were found to be significantly non-random for the *C. ponderosae* networks (Tables 3.6-3.8). Testing those significant clades with the inference key outlined by Templeton yielded in six of those results yielding informative results (Table 3.10). The network of *C. edulis* had five significant geographical associations (Table 3.9), with four of those being informative with the inference key (Table 3.10).

Discussion

Two different patterns emerged from the nested clade analysis of *C. ponderosae* and *C. edulis*. In the case of *C. ponderosae,* multiple lineages evolved independently to utilize *P. ponderosa* and other western pines as hosts, including both yellow and white pines. The three *C. ponderosae* haplotype networks were isolated by at least nine mutational steps, suggesting that there has been a long time of separation for these clades.

There is at least 1.2% sequence divergence, which equates to approximately 500,000 years, given a approximate nucleotide substitution rate of 2.3% per million years for arthropods (Brower 1994). This is significant because the migration of *P. ponderosa* into northern America did not occur until 12-8,000 years before present (Conkle and Critchfield 1988, Axelrod 1986), so separation of these clades preceded the current distribution of pines since at least the last glacial maximum.

Second, the three lineages of *C. ponderosae* appear to have unique histories according to the nested clade analysis. Group 1 (Figure 3.2), which encompasses individuals from the southwest and includes individuals that feed on white pines (*P. strobiformis*), has a history of past fragmentation and/or long distance colonization for all of the individuals sampled. Within those haplotypes, there are two groups of haplotype lineages: one that is experiencing continguous range expansion and the other experiencing restricted gene flow with some long distance dispersal (Table 3.10). The individuals sampled in the groups one and three encompass a range of localities (Tables 3.2 and 3.4), which represent "island" pine populations that are isolated by distance. Individual stands of pines produce cones in a cyclic nature, with abundant crops every 4 years (Jenkins, 1984). However, different stands "peak" at different times, which influences the distribution of cone-feeding insects (Jenkins 1984). So not only are pine cone beetles affected by the local patterns of cone production, but also distances between stands of trees. The populations sampled that exhibit range expansion include all of the individuals from Taos Co. New Mexico and from Ashley National Forest in Dagget Co. Utah in group 1 (Tables 3.2 and 3.10), which may represent more recent invasions into those forest habitats or expansion of the pines in that area and the subsequent movement

of the beetles. Unfortunately it is not possible to test alternate hypotheses generated by NCA (Knowles and Maddison, 2002), so differentiating between the two is not possible.

There were significant results for nested clade analysis groups 2 and 3 (Table 3.10), but both are affected by sampling. Both groups have many missing haplotypes, which may include the "true" ancestral haplotype. Coalescence theory predicts that the most common haplotype is the ancestral haplotype which could be an erroneous assumption given the limited sample size for these groups. For example, if sampling does not occur near the origin of the haplotype lineage, then more derived haplotypes may be sampled as compared to "ancestral" haplotypes (Knowles and Maddison 2005). These common derived haplotypes would be assumed "ancestral". In the case of Group 2, only a first level grouping was found to have a significant result (Table 3.7), and range expansion was suggested by the inference key (Table 3.10). This group includes individuals from the Northwest, and only two populations were sampled (Table 3.1). This area is believed to have the most recent colonization of *P. ponderosae* (Conkle and Critchfield 1988), and as a result the beetles may have also recently arrived to the area. However, there are sampling gaps and if filled would allow for a better estimate of gene flow. Group 3 had a similar problem, but only higher level associations were significant. Both 4-1, which includes most individuals from the southwest and some from Mexico, and all of the individuals in this group were found to have restricted gene flow with isolation by distance. The isolation by distance conclusion may be due to the sampling gap between central Mexico and Southern Arizona, or the patchy distribution of pine forests in the southwest. Increased sampling within this gap could clarify this issue.

Overall multiple factors appear to affect population substructure of *C. ponderosae*. While increased sampling would help to confirm these conclusions, there are some trends that appear to be linked to their host. For one, many of the white and yellow pines of the southwest are recent re-colonizers of northern America as recently as 12,000 years ago (Axelrod 1986, Van Devender 1990a, 1990bn). As a result there may not have been enough time for mtDNA lineage sorting to occur for herbivores that feed on this host.

Second, many of the pine forests, particularly in the arid southwest are isolated as "islands" at higher altitudes (Van Devender 1990a, 1990b). This island isolation has affected population genetic structure of other organisms (Kelley et al. 1999, Smith and Farrell 2005, Wilson et al. 2005) and may be responsible for the genetic structure among *Conophthorus* haplotype lineages. For example, in the case of the mountain cricket *Melanoplus,* it was found that there was a recolonization of mountain habitats that were covered by icesheets during the Pleistocene (Knowles 2001a), and this movement helped in the radiation of at least one species, *M. oregonensis* (Knowles 2001b). Interestingly, paraphyly of mtDNA haplotypes was also observed for this genus and was attributed to the colonization of these areas by ancestral populations (Knowles 2001a). However, morphological differences, particularly the genitalia provide evidence for species monophyly (Knowles 2001a). *Conophthorus*, unlike *Melanoplus*, is alate and has a much larger distribution (Wood and Bright 1992), so there is increased potential for gene flow and a potentially larger effective population size. As a result, if lineage sorting has not occurred even on a flightless insect with reduced gene flow following the Pleistocene,

Conophthorus may present a system that is too complex to adequately show phylogeographical resolution in such a short period.

In the case of *C. edulis*, the nested clade analysis suggests a history of range expansion and contraction. There is a pattern of restricted gene flow followed by continuous range expansion of the haplotypes. This also appears consistent with the history of their host, the pinyon pines (*P. edulis, P. cembroides*). Tracks of pinyon pines and juniper existed throughout North American in lower elevations, from the Wisconsin period until as recent as 12,000 ya. During the brief warming periods during this ice-age (Webb and Bartlein 1992) the pinyon and juniper forests retreated to higher elevations (Van Derender 1990a,1990b), and created more isolated, island like habitats. Populations of *C. edulis* associated with those pines also were likely isolated in a patchy tree distribution. During the colder periods, the pines move to lower elevations (Van Derender 1986, Bentacourt et al. 1991) and probably re-established contact among beetle populations. After around 12,000 ybp, as the climate dried and warmed, pinyon pines and junipers retreated to their current range of isolated patches in higher altitudes in the southwestern United States and Mexico (Axelrod 1986, Van Derender 1986, Bentacourt et al. 1991).

Unlike *P. ponderosa* and the other western pines, the pinyon pines (*P. edulis* and *P. cembroides*) have been present in the Mexican and North American fauna for at least 30,000 years (Axelrod 1986, Van Derender 1990a, 1990b, Spaulding 1990). As a result, lineages of beetles that feed on these trees would have had more time to experience geographical population substructuring than those that feed on hosts still expanding in their range. This is reflected in the nested clade analysis. The populations of *C. edulis*

exhibit geographic structure at all levels of haplotype groupings. These associations suggest that lineage diversification may occur by allopatric separation. *C. ponderosae,* on the other hand, has significant structuring only on the higher levels of groupings. Although this could be due to sampling shortcomings, host use may influence lineage diversification and population substructuring. *C. ponderosae* lineages exhibit association with particular hosts within certain geographic areas (Chapter II).

CHAPTER IV

CONCLUSION

The Pleistocene had an impact on much of the fauna in North America, including *Conophthorus*. With the long cold periods and short warm periods, faunas shifted in latitude and altitude with the changing environments. This movement included the hosts of many *Conophthorus* species. In the case of *C. edulis*, its main host, the Colorado pinyon pine, was present in the low altitudes of Mexico and the southwestern United States at least 30,000 years ago. During this period the ranges expanded and contracted as the climate became more arid and rainfall amounts changed, but these pines were continually presence in the southwest. This is reflected in the population structure of *C. edulis.* There is more population structure for all levels of groupings of haplotypes tested by nested clade analysis, suggesting that the species was also present in the southwestern United States for a relatively longer period of time to develop this structure.

Unlike many of the pinyon pines, which have been in North America for at least 30,000 years, *Pinus ponderosa* and other western yellow and white pines have only recently migrated into northern America about 8,000 years ago. Because of this recent expansion, *Conophthorus ponderosae*, the species that feeds on most of these pines, also probably expanded rapidly with its host. This is reflected in the nested clade analysis. There are three haplotype networks, indicating that there have been at least three lineages that have diversified with the use of *P. ponderosa*. Two of these lineages overlap in their geographical ranges despite having diverged at least 500,000 years before present, which suggests allopatric divergence at more southern latitudes. Second, there is little recent population structure for many of the networks, and only higher-level groupings correlate

with geography. While this could be due again to the brief period of the current hosts range, other factors such as local adaptation to host use may be a factor (Chapter I). However, distinguishing between these factors will continue to be problematic despite increased sampling efforts for this species.

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APPENDIX A

TABLES

Table 2.1. Number of individuals per species sampled for mtDNA analysis per locality. Individuals were collected from separate pine cones.

Species	Population locality	Host	# of ind.
C. edulis	New Mexico: Ortero Co.	*Pinus edulis*	10
C. edulis	Mexico: Coahuila	*Pinus cembroides*	10
C. coniperda	North Carolina: Cherokee Co.	*Pinus strobus*	10
C. edulis	Utah: Grand Co.	*Pinus edulis*	10
C .conicolens	Mexico	*Pinus leiophylla*	8
C. edulis	Mexico: Queretaro.	*Pinus cembroides*	7
C. edulis	Colorado: Chaffee Co.	*Pinus edulis*	2
C. edulis	Colorado: Dolores Co.	*Pinus edulis*	10
C. edulis	New Mexico: Cibola Co.	*Pinus edulis*	9
C. edulis	Mexico: Queretaro	*Pinus cembroides*	9
C. edulis	Utah: Duchesne Co.	*Pinus edulis*	1
C. mexicanus	Mexico: Puebla	*Pinus patula*	5
C. sp	Mexico: Mexico	*Pinus leiophylla*	3
C.ponderosae	Utah: Dagget Co. Ashley NF	*P.ponderosa*	10
C.ponderosae	Utah: Washington Co.	*P.ponderosa*	10
C.ponderosae	Arizona: Coconino Co.	*P.ponderosa*	10
C.ponderosae	Nevada: Clark Co.	*P.ponderosa*	10
C.ponderosae	New Mexico: Taos Co.	*P.ponderosa*	10
C.ponderosae	Colorado: Larimer Co.	*P.ponderosa*	8
C.ponderosae	Colorado: Saguache Co.	*P.ponderosa*	9
C.ponderosae	New Mexico: Colfax Co.	*P.ponderosa*	9
C.ponderosae	Nevada: Clark Co.	*P.flexilis*	1
C.ponderosae	Utah: Dagget Co. Ashley NF	*P.flexilis*	1
C.ponderosae	Arizona: Cochise Co. Chiricahua Mts.	*P.arizonica*	10
C.ponderosae	Arizona: Graham Co. Pinaleno Mts.	*P.strobiformis*	9
C.ponderosae	Arizona: Graham Co. Pinaleno Mts.	*P.arizonica*	3
C.ponderosae	Arizona: Pima Co. St. Catalina Mts	*P.strobiformis*	10
C.ponderosae	Arizona: Pima Co. St. Catalina Mts	*P.arizonica*	10
C.ponderosae	Arizona: Cochise Co. Chiricahua Mts.	*P.leiophylla*	2
C.ponderosae	Arizona: Pima Co. St. Catalina Mts	*P.strobiformis*	5
C.ponderosae	Mexico: Mexico	*P.hartwegii*	2
C.ponderosae	New Mexico: Ortero Co.	*P.arizonica*	8
C.ponderosae	New Mexico: Cibola Co.	*P.ponderosa*	2
C.ponderosae	Oregon: Wasco Co.	*P.ponderosa*	8
C.ponderosae	Idaho: Idaho Co.	*P.ponderosa*	5
C.apachecae	Mexico: Durango	*P.engelmanni*	1
C.conicolens	Mexico: Michoacan	*P.pseudostrobus*	1
C.coniperda	Maryland: Anne Arundal Co.	*P.strobus*	1
C.coniperda	New York: Suffolk Co.	*P.strobus*	1
C.coniperda	Rhode Island: Lincoln Co.	*P.strobus*	1
C.coniperda	West Virginia: Pendleton Co.	*P.rigida*	1
C.coniperda	Canada: Ontario	*P.strobus*	1

Table 2.1 continued

Species	Population locality	Host	# of ind.
C.echinate	Missouri: Carter Co.	*P.echinata*	1
C.edulis	Utah: Kane Co.	*P.edulis*	1
C.edulis	Arizona: Cochise Co.	*P.cembroides*	1
C.edulis	Mexico: Hidalgo	*P.cembroides*	1
C. michoacanae	Mexico: Michoacan	*P.michoacana*	1
C.mexicanus	Mexico: Hidalgo	*P.patula*	1
C.monophyllae	California: Riverside Co.	*P.monophylla*	1
C.ponderosae	California: Calaveras Co.	*P.ponderosa*	1
C.ponderosae	California: Siskiyou Co.	*P.ponderosa*	1
C.ponderosae	Idaho: Bonner Co.	*P.ponderosa*	1
C.ponderosae	Idaho: Kootenai Co.	*P.monticola*	1
C.ponderosae	Canada: British Columbia	*P.monticola*	1
C.ponderosae	Canada: British Columbia	*P.contorta*	1
C.ponderosae	Canada: British Columbia	*P.monticola*	1
C.ponderosae	California: El Dorado Co.	*P.lamberitana*	1
C.ponderosae	California: Mendicino Co.	*P.lamberitana*	1
C.ponderosae	California: Riverside Co.	*P.ponderosa*	1
C.ponderosae	California: San Bernardino Co.	*P.ponderosa*	1
C.ponderosae	California: Fresno Co.	*P.lamberitana*	1
C.ponderosae	California: Riverside Co.	*P.lamberitana*	1
C.ponderosae	Mexico: Baja California	*P.lamberitana*	1
C.ponderosae	Arizona: Coconino Co.	*P.arizonica*	1
C.ponderosae	Nevada: White Pine Co.	*P.flexilis*	1
C.ponderosae	Colorado: Park Co.	*P.aristata*	1
C.ponderosae	Nevada: Clark Co.	*P.arizonica*	1
C.ponderosae	Mexico: Durango	*P.arizonica*	1
C.ponderosae	Mexico: Mexico	*P.hartwegii*	1
C.radiatae	California: Alameda Co.	*P.radiata*	1
C.radiatae	Canada: Ontario	*P.banksiana*	1
C.resinosae	Canada: Ontario	*P.resinosa*	1
C.teocotum	Mexico: Michoacan	*P.teocote*	1
C.terminalis	Mexico: Nuevo Leon	*not recorded*	1
C.sp2	Mexico: Mexico	*P.leiophylla*	1
C.sp3	Mexico: Mexico	*P.montezumae*	1
Dendroterus striatus	California: San Diego Co.	*Bursera microphylla*	1
Pityophthorus setosus	California: Monterey Co.	*P.radiata*	1
Pseudopytyophthorus setosus	California: Alameda Co.	*Quercus sp.*	1
Pseudopytyophthorus pruinosus	New York: Suffolk Co.	*Quercus sp.*	1

Table 2.2. Associations between *Conophthorus ponderosae* lineages, hosts and geographic regions. First number in each column is Monte Carlo significance, followed by standard error * significantly different from random at p<0.01. First comparison considers *C. ponderosae* ESCs and all geographic areas. The remaining comparisons only consider associations within specific areas. NA= Not Applicable. ESCs are defined in text and Appendix C.

				Area	**Area**
		host subgenera	host subsections	200- 300 km	> 900 km
	ESC	0.057, 0.007	0.139, 0.011	< 0.001, < 0.001*	0.003, 0.002*
Within area M, >900 km	ESC	< 0.001, < 0.001*	< 0.001, < 0.001*	NA	NA
Within area S, >900 km	ESC	0.14, 0.011	< 0.001, < 0.001*	NA	NA
Within area E, >900 km	ESC	1.0, 0.0	< 0.001, < 0.001*	NA	NA

Table 3.1. Numbers of individuals and localities sampled for populations of *C. edulis* and *C. ponderosae* in nested clade analysis. Coordinates are either in minutes or degrees depending on the GPS unit used during specimen collection.

Species	Population locality	Coordinates	Host	#
C. edulis	New Mexico: Ortero Co.	32.9493N 105.8326W	*Pinus edulis*	10
C. edulis	Mexico: Coahuila	N/A	*Pinus cembroides*	10
C. edulis	Utah: Grand Co.	38.5040N 109.3267W	*Pinus edulis*	10
C. edulis	Mexico: Queretaro.	20.53.039N 99.39.513N	*Pinus cembroides*	7
C. edulis	Colorado: Chaffee Co.	38.38.161N 106.04.873W	*Pinus edulis*	2
C. edulis	Colorado: Dolores Co.	37.6747N 108.6928W	*Pinus edulis*	10
C. edulis	New Mexico: Cibola Co.	35.4452N 108.5491W	*Pinus edulis*	9
C. edulis	Mexico: Queretaro	21.10.64N 99.45.704W	*Pinus cembroides*	1
C. edulis	Utah: Duchesne Co.	40.08N 110.29W	*Pinus edulis*	1
C.ponderosae	Utah: Dagget Co. 1	40.53N 109.34W	*P.ponderosa*	10
C.ponderosae	Utah: Washington Co.	37.22N 113.28W	*P.ponderosa*	10
C.ponderosae	Arizona: Coconino Co.	36.46N 112.16W	*P.ponderosa*	10
C.ponderosae	Nevada: Clark Co.	36.16N 115.41W	*P.ponderosa*	10
C.ponderosae	New Mexico: Taos Co.	36.41.929N 105.28.956W	*P.ponderosa*	10
C.ponderosae	Colorado: Larimer Co.	40.2682N 105.3966W	*P.ponderosa*	8
C.ponderosae	Colorado: Saguache Co.	38.07.392N 106.29.361W	*P.ponderosa*	9
C.ponderosae	New Mexico: Colfax Co.	36.58.433N 104.23.627W	*P.ponderosa*	9
C.ponderosae	Nevada: Clark Co.	36.19N 115.41W	*P.flexilis*	1
C.ponderosae	Utah: Dagget Co.2	39.54N 110.43W	*P.flexilis*	1
C.ponderosae	Arizona: Cochise Co. 1	31.91739N 109.27934W	*P.arizonica*	10
C.ponderosae	Arizona: Graham Co. 1	32.62936N 109.82687W	*P.strobiformis*	9
C.ponderosae	Arizona: Graham Co. 2	32.71622N 109.94026W	*P.arizonica*	3
C.ponderosae	Arizona: Pima Co. 1	32.41575N 110.73651W	*P.strobiformis*	10
C.ponderosae	Arizona: Pima Co. 2	32.38462N 110.69379W	*P.arizonica*	10
C.ponderosae	Arizona: Cochise Co. 2.	31.78348N 109.83587W	*P.leiophylla*	2
C.ponderosae	Arizona: Pima Co. 3	32.62717N 109.83587W	*P.strobiformis*	5
C.ponderosae	Mexico: Mexico	19.05.053N 98.38.876W	*P.hartwegii*	2
C.ponderosae	New Mexico: Ortero Co.	32.9601N 105.7737W	*P.arizonica*	8
C.ponderosae	New Mexico: Cibola Co.	35.4145N 108.5491W	*P.ponderosa*	2
C.ponderosae	Oregon: Wasco Co.	45.40N 121.20W	*P.ponderosa*	8
C.ponderosae	Idaho: Idaho Co.	45.91N 116.12W	*P.ponderosa*	5

Table 3.2. Numbers of individuals and their given localities for each of the haplotypes found in Group 1 haplotype network of *C. ponderosae* (Figure 3.2).

Haplotype	(# individuals) Population
A	(2) Pine Valley, Dagget Co.UT, (3) Cococino Co. AZ, (1) Colfax Co. NM
B	(7) Saguache Co. CO
C	(4) Graham Co. AZ 1, (4) Pima Co. AZ 3.
D	(9) Pima Co. AZ 1
E	(9) Ashley, Dagget Co. UT 1, (1) Taos Co. NM, (1) Ashley, Dagget Co. UT 2.
F	(2) Taos Co. NM, (2) Larimer Co. CO, (5) Colfax Co. NM.
G	(2) Colfax Co. NM
H	(1) Graham Co. AZ 1
I	(1) Graham Co. AZ 1
J	(2) Graham Co. AZ 1
K	(1) Saguache Co. CO
L	(1) Saguache Co. CO
M	(1) Cococino Co. AZ
N	(1) Larimer Co. CO
O	(1) Ashley, Dagget Co. UT 1
P	(1) Graham Co. AZ 1
Q	(1) Pima Co. AZ 1
R	(1) Mexico, Mexico
S	(1) Ortero Co. NM
T	(1) Taos Co. NM
U	(1) Taos Co. NM

Table 3.3. Numbers of individuals and their given localities for each of the haplotypes found in Group 2 haplotype network of *C. ponderosae* (Figure 3.3).

Haplotype	(# individuals) Population
IX	(3) Wasco Co. OR
X	(1) Wasco Co. OR, (5) Idaho Co. ID
XI	(1) Wasco Co. OR
XII	(1) Wasco Co. OR
XIII	(1) Wasco Co. OR
XIV	(1) Wasco Co. OR

Table 3.4. Numbers of individuals and their given localities for each of the haplotypes found in Group 3 haplotype network of *C. ponderosae* (Figure 3.4).

Haplotype	(# individuals) Population
XV	(1) Pine Valley, Dagget Co. UT, (9) Clark Co. NV 1 (1) Taos Co. NM, (4) Larimer Co. CO, (1) Colfax Co. NM, (2) Graham Co. AZ 2.
XVI	(5) Cochise Co. AZ 1 (6) Pima Co. AZ 2, (2) Cochise Co. AZ 2
XVII	(1) Cochise Co. AZ 1
XVIII	(1) Cochise Co. AZ 1
XIX	(1) Cochise Co. AZ 1
XX	(1) Cochise Co. AZ 1
XXI	(2) Pima Co. AZ 2.
XXII	(1) Cochise Co. AZ 1
XXIII	(1) Pima Co. AZ 2
XXIV	(1) Clark Co. NV
XXV	(1) Graham Co. AZ 2
XXVI	(1) Ortero Co. NM
XXVII	(1) Ortero Co. NM
XXVIII	(1) Taos Co. NM.
XXIX	(1) Larimer Co. CO
XXX	(1) Clark Co. NV 3
XXXI	(1) Ortero Co. NM
XXXII	(1) Cibola Co. NM
XXXIII	(1) Cibola Co. NM
XXXIV	(1) Ashley, Dagget Co. UT 1
XXXV	(2) Ortero Co. NM
XXXVI	(1) Ortero Co. NM
XXXVII	(1) Ortero Co. NM
XXXVIII	(1) Ortero Co. NM
XXXIX	(1) Pima Co. AZ 2
XXXX	(4) Clark Co. NV 1, (2) Taos Co. NM
XXXXI	(1) Clark Co. NV 1
XXXXII	(1) Clark Co. NV 1
XXXXIII	(1) Taos Co. NM.
XXXXIV	(1) Mexico, Mexico

Table 3.5. Numbers of individuals and their given localities for each of the haplotypes found in the *C. edulis* haplotype network (Figure 3.1).

Haplotype	(# individuals) Population
A	(3) Grand Co. UT, (4) Dolores Co. CO, (3) Queretaro Mexico, (4) Cibola Co. NM
B	(1) Cibola Co. NM
C	(1) Duchesne Co. UT
D	(1) Grand Co. UT
E	(1) Ortero Co. NM, (4) Cibola Co. NM, (4) Grand Co. UT, (1) Dolores Co. UT, (1) Queretaro Mexico
F	(1) Dolores Co. CO
G	(2) Ortero Co. NM, (1) Cuahuila Mexico, (2) Queretaro Mexico
H	(1) Grand Co. UT
I	(2) Dolores Co. CO, (1) Queretaro Mexico
J	(1) Queretaro Mexico
K	(5) Cuahuila Mexico (4) Queretaro Mexico
L	(1) Grand Co. UT
M	(2) Cuahuila Mexico
N	(1) Ortero Co. NM
O	(1) Ortero Co. NM, (2) Cuahuila Mexico, (1) Queretaro Mexico
P	(4) Ortero Co. NM, (2) Queretaro Mexico (1) Dolores Co. CO, (1) Queretaro 2 Mexico
Q	(1) Chaffee Co. CO
R	(1) Dolores Co. CO
S	(1) Ortero Co. NM
T	(1) Chaffee Co. CO

Table 3.6. Permutational chi-square statistics and probability of a random distribution of haplotypes across the geographical range of *C. ponderosae* haplotypes in group 1. Significant values (>5%) are demarcated by *.

Group 1 *C. ponderosae* network

Clade	Permutational chi-square statistic	Probability
1-4	18.37	0.220
1-7	0.75	1.000
1-9	3.00	0.318
1-10	17.31	0.000*
1-11	3.00	1.000
2-2	115.15	0.000*
2-3	14.77	0.016*
Entire cladogram	126.76	0.000*

Table 3.7. Permutational chi-square statistics and probability of a random distribution of haplotypes across the geographical range of *C. ponderosae* haplotypes in group 2. Significant values (>5%) are demarcated by *.

Group 2 *C. ponderosae* network

Clade	Permutational chi-square statistic	Probability
1-2	6.67	0.048*
2-1	0.92	1.000
3-1	0.78	1.000
Entire cladogram	0.83	1.000

Table 3.8. Permutational chi-square statistics and probability of a random distribution of haplotypes across the geographical range of *C. ponderosae* haplotypes in group 3. Significant values (>5%) are demarcated by *.

Group 3 *C. ponderosae* network

Clade	Permutational chi-square statistic	Probability
1-1	29.62	0.321
1-13	2.69	0.807
1-14	2.00	1.000
1-17	25.67	0.134
2-2	1.88	1.000
2-6	5.10	0.591
2-8	35.45	0.071
3-1	2.43	0.583
3-2	13.04	0.504
4-1	0.00	0.000*
Entire cladogram	0.00	0.000*

Table 3.9. Permutational chi-square statistics and probability of a random distribution of haplotypes across the geographical range of *C. edulis* haplotypes. Significant values (>5%) are demarcated by *.

C. edulis haplotype network

Clade	Permutational chi-square statistic	Probability
1-1	19.43	0.0250*
1-5	7.04	0.648
1-7	1.53	1.000
1-9	2.00	1.000
2-1	50.3963	0.0010*
2-2	6.3462	0.3300
3-2	42.7610	0.0360*
Entire cladogram	14.8977	0.0520

Table 3.10. Inference key results for the significant clades in the Geodis 2.0 analysis.

Group 1 *C. ponderosae* nested clade inference key results	
Clade	
1-10	Inconclusive outcome
2-2	Restricted gene flow with some long distance dispersal
2-3	Contiguous range expansion
3-1	Past fragmentation an/or long distance colonization

Group 2 *C. ponderosae* nested clade inference key results	
Clade	
1-17	Contiguous range expansin

Group 3 *C. ponderosae* nested clade inference key results	
Clade	
4-1	Restricted Gene flow with Isolation by Distance
6-1	Restricted Gene flow with Isolation by Distance

***C. edulis* nested clade inference key results**	
Clade	
1-1	Restricted Gene flow with Isolation by distance
1-3	Restricted Gene flow with Isolation by distance
2-1	Inconclusive outcome
3-2	Contiguous range expansion
4-1	Restricted Gene flow with Isolation by distance

Table 3.11. Localities corresponding to Figure 2.5 of *Conophthorus ponderosae.*

Number	Population	Host	# of Ind.
1	Utah: Dagget Co. Ashley NF 1	*P.ponderosa*	10
2	Utah: Dagget Co. Pine Valley	*P.ponderosa*	10
3	Arizona: Coconino Co.	*P.ponderosa*	10
4	Nevada: Clark Co.1	*P.ponderosa*	10
5	New Mexico: Taos Co.	*P.ponderosa*	10
6	Colorado: Larimer Co.	*P.ponderosa*	8
7	Colorado: Saguache Co.	*P.ponderosa*	9
8	New Mexico: Colfax Co.	*P.ponderosa*	9
9	Nevada: Clark Co2.	*P.flexilis*	1
10	Utah: Dagget Co. Ashley NF 2	*P.flexilis*	1
11	Arizona: Conchise Co. Chiricahua Mts.1	*P.ponderosa*	10
12	Arizona: Graham Co. Pinaleno Mts.1	*P.strobiformis*	9
13	Arizona: Graham Co. Pinaleno Mts.2	*P.ponderosa*	3
14	Arizona: Pima Co. St. Catalina Mts.1	*P.strobiformis*	10
15	Arizona: Pima Co. St. Catalina Mts.2	*P.ponderosa*	10
16	Arizona: Conchise Co. Chiricahua Mts.2	*P.leiophylla*	2
17	Arizona: Pima Co. St. Catalina Mts.3	*P.strobiformis*	5
18	Mexico: Mexico	*P.hartwegii*	2
19	New Mexico: Ortero Co.	*P.ponderosa*	8
20	New Mexico: Cibola Co.	*P.ponderosa*	2
21	Oregon: Wasco Co.	*P.ponderosa*	8
22	Idaho: Idaho Co.	*P.ponderosa*	5

Table 3.12. Localities corresponding to Figure 2.6 of *Conophthorus edulis.*

Number	Population	Host	# of Individuals
1	Utah: Grand Co.	*P. edulis*	10
2	Colorado: Dolores Co.	*P. edulis*	10
3	Mexico: Queretaro.	*P. cembroides*	7
4	New Mexico: Cibola Co.	*P. edulis*	9
5	Utah: Duchesne Co.	*P. edulis*	1
6	New Mexico: Ortero Co.	*P. edulis*	10
7	Mexico: Coahuila	*P. cembroides*	10
8	Mexico: Queretaro 2.	*P. cembroides*	9
9	Colorado: Chaffee Co.	*P. edulis*	2

APPENDIX B

FIGURES

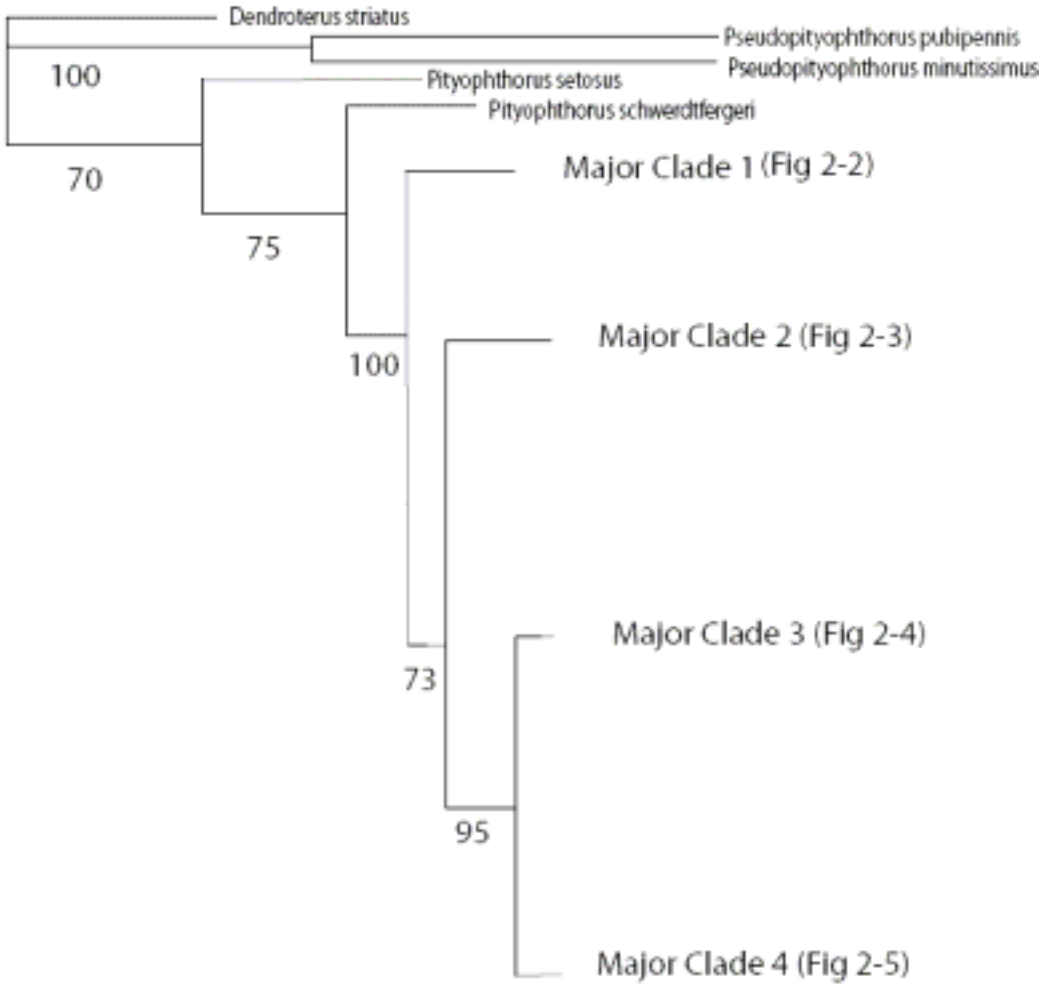

Figure 2.1 Consensus of phylogeny of *Conophthorus* using one equally parsimonious tree of 13,200 trees based on 751bp of mtDNA. Bootstrap values for all nodes over 50% are indicated by their respective nodes. The CI and RI values are 0.612 and 0.892, respectively. Locality and number of individuals sharing each haplotype are in parenthesis. Individual haplotypes within the major clades are in Figures 2.2. through 2.5.

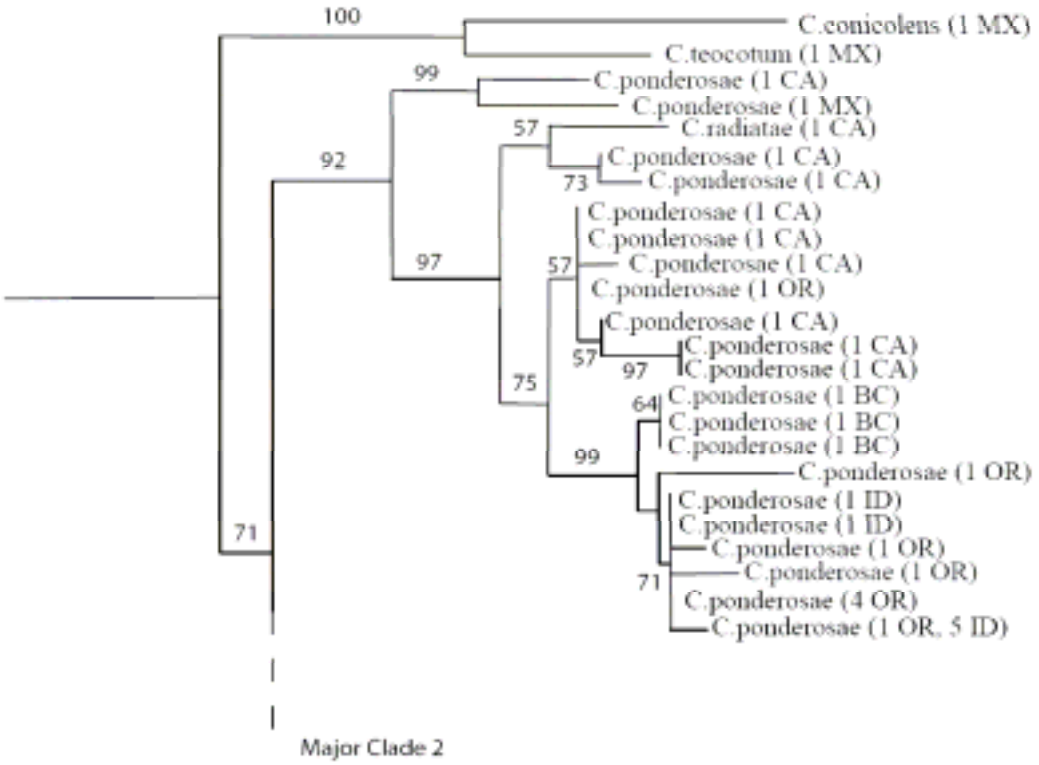

Figure 2.2 Individual haplotypes found in Major Clade one of four in Figure 2.1. The species name has the number of individuals with that haplotype from each locality. Nodes with greater than 50% bootstrap values are demarcated with their respective values.

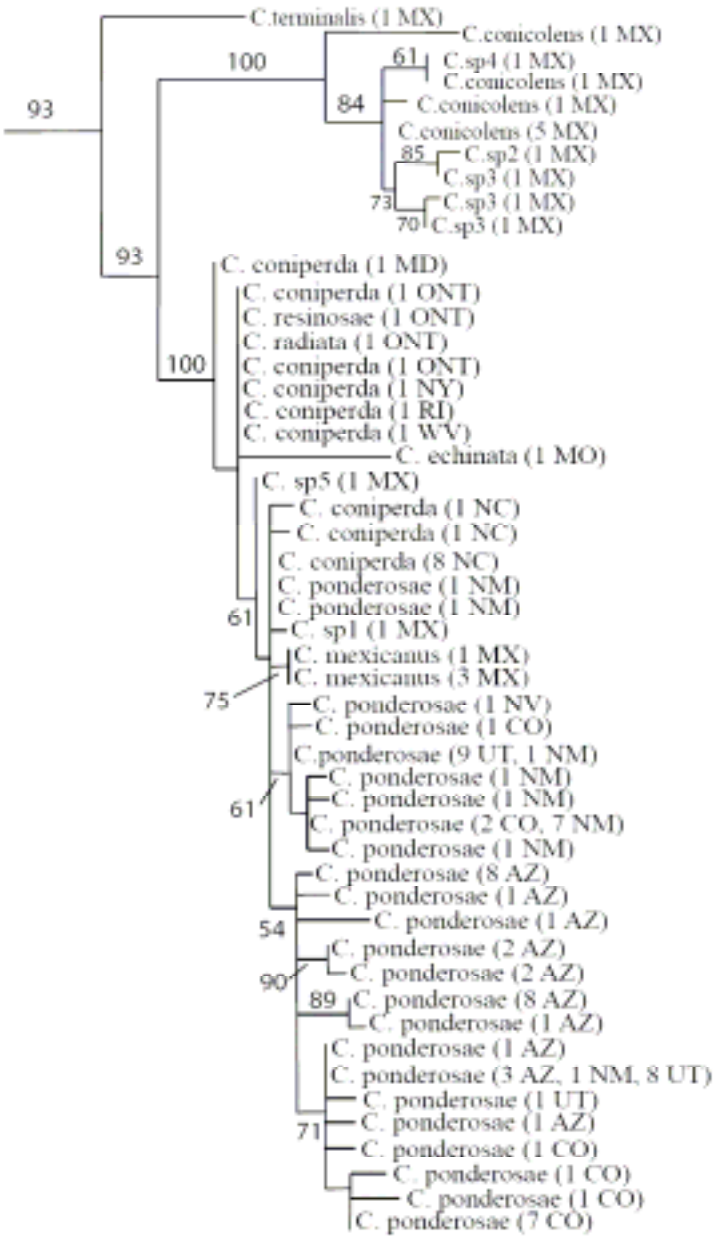

Figure 2.3 Individual haplotypes found in Major Clade two of four in Figure 2.1. The species name has the number of individuals with that haplotype from each locality. Nodes with greater than 50% bootstrap values are demarcated with their respective values.

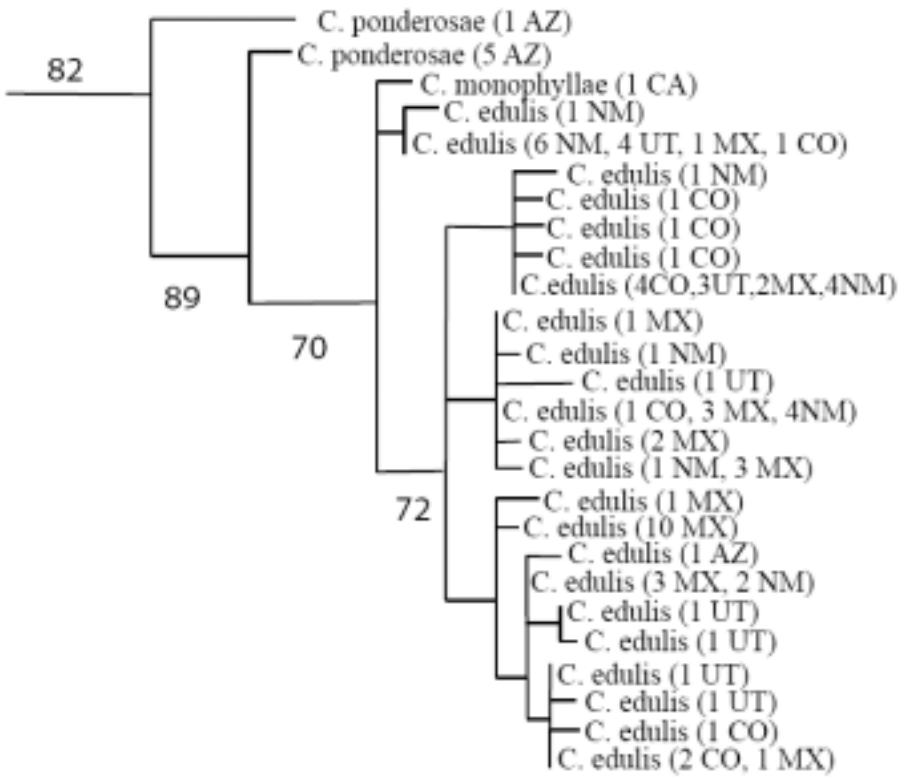

Figure 2.4 Individual haplotypes found in Major Clade three of four in Figure 2.1. The species name has the number of individuals with that haplotype from each locality. Nodes with greater than 50% bootstrap values are demarcated with their respective values.

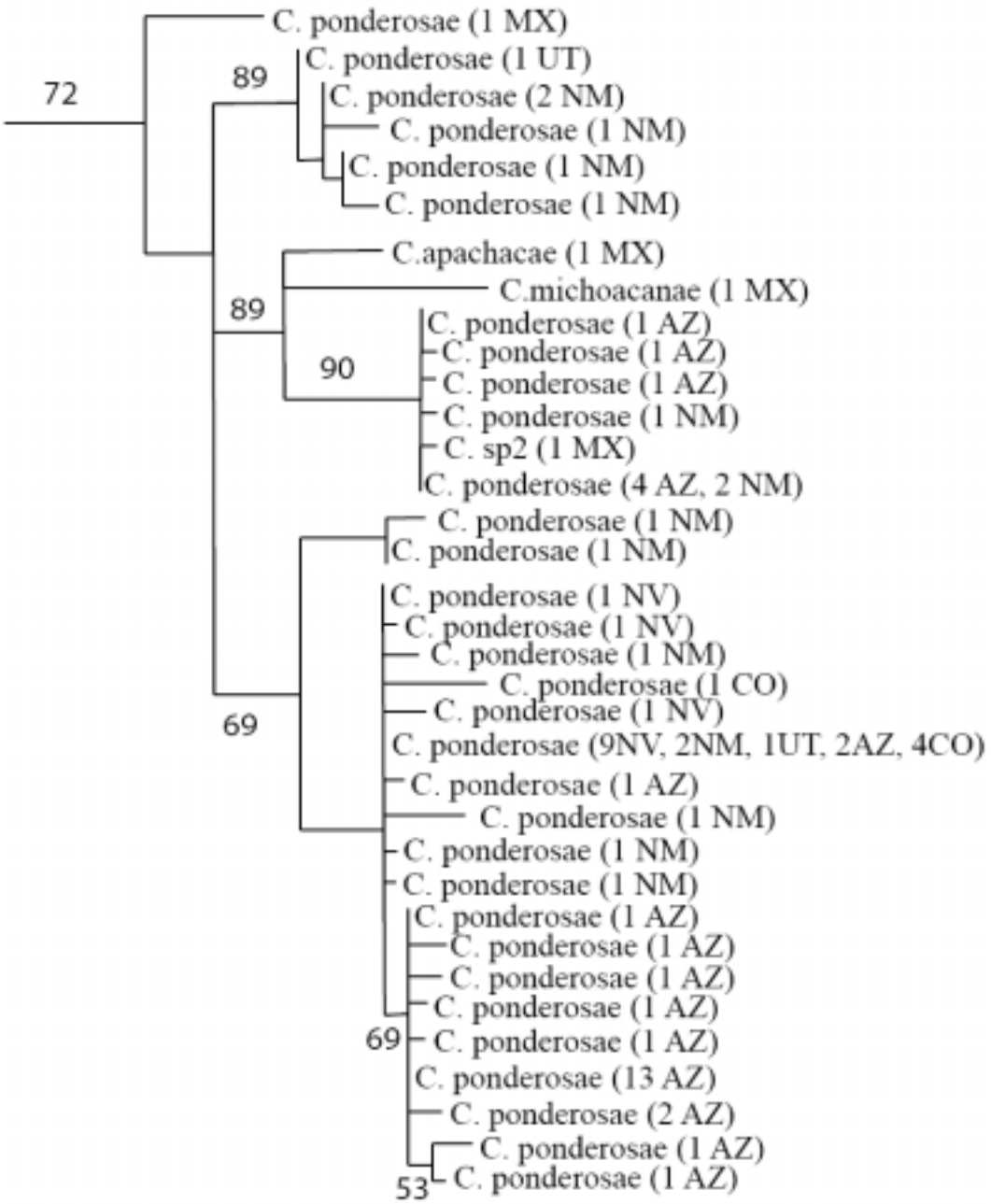

Figure 2.5 Individual haplotypes found in Major Clade four of four in Figure 2.1. The species name has the number of individuals with that haplotype from each locality. Nodes with greater than 50% bootstrap values are demarcated with their respective values.

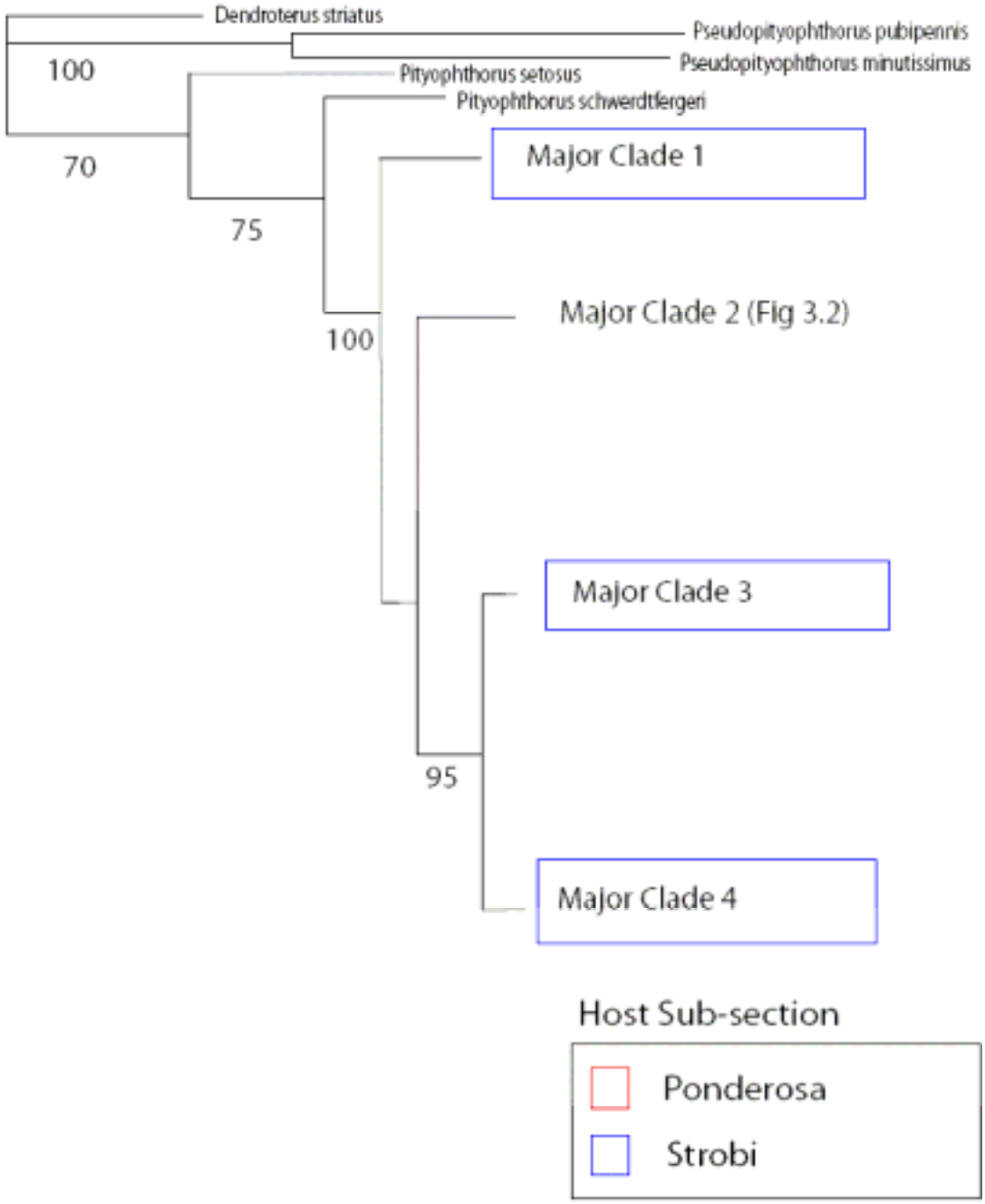

Figure 2.6. Host use among individuals sampled of *Conophthorus*. Sub-sections of *Pinus* are indicated by boxes around the taxa.

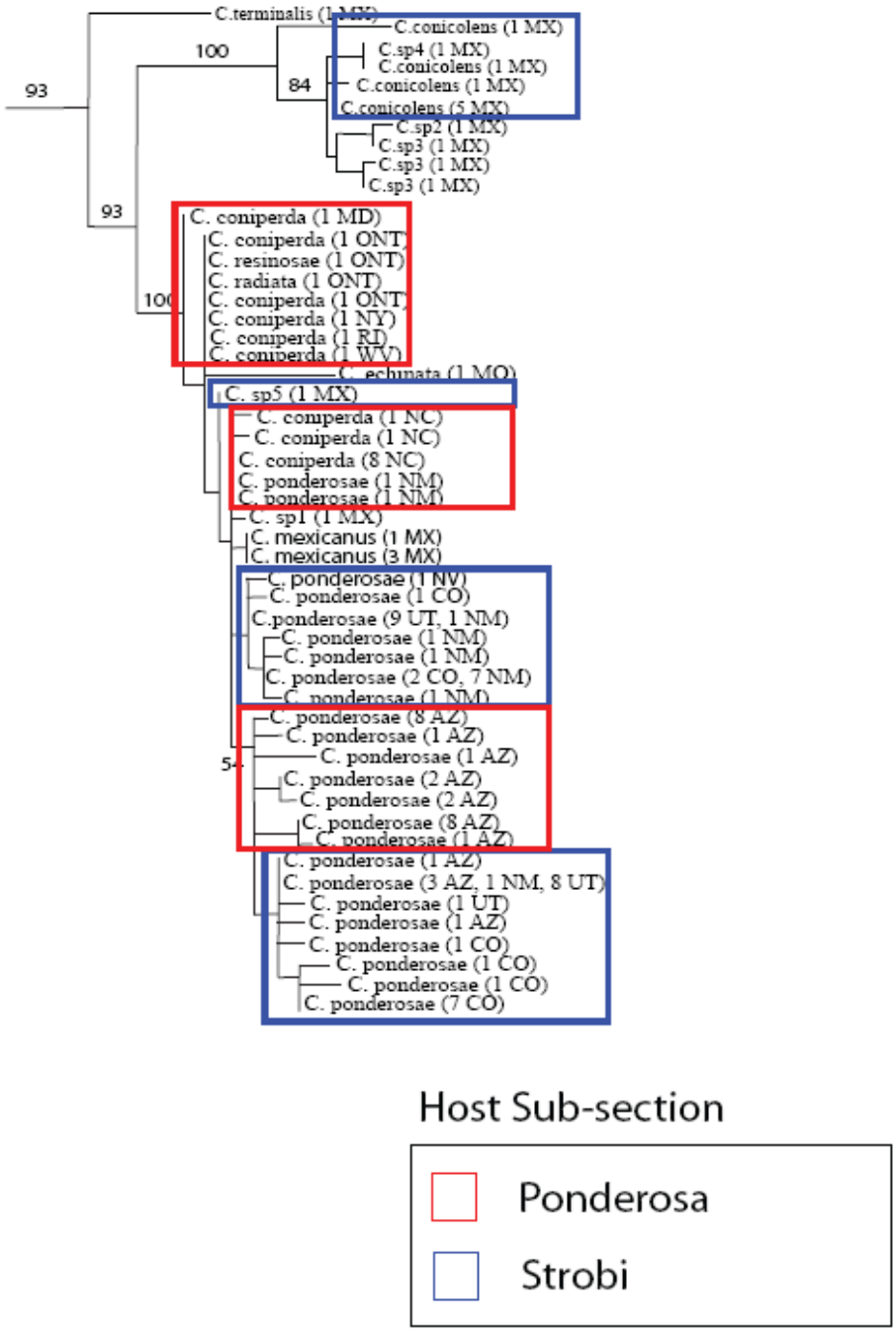

Figure 2.7. Host use among individuals sampled of *Conophthorus* in Major Clade 2. Sub-sections of *Pinus* are indicated by boxes around the taxa.

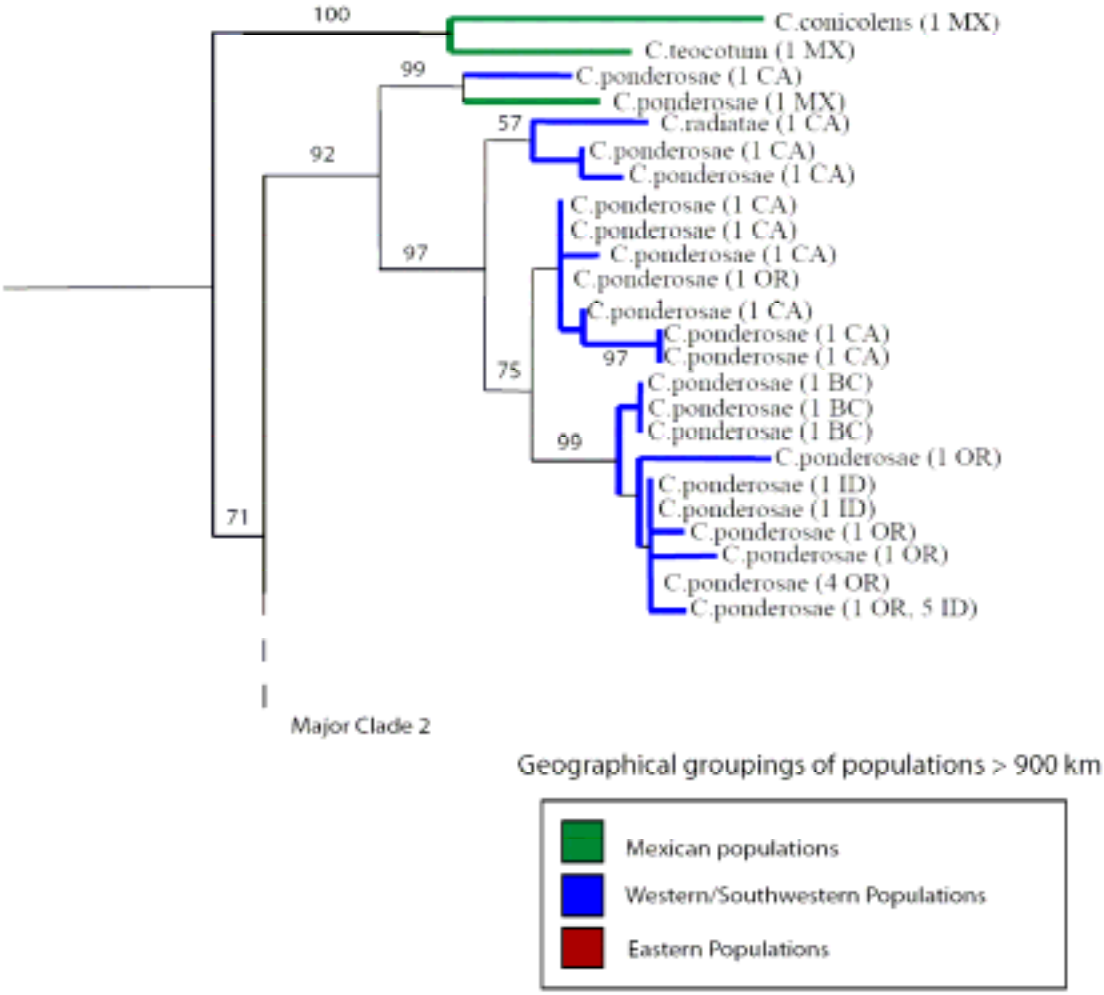

Figure 2.8. Geographic association of haplotypes of *Conophthorus* individuals sampled in major group one. Geographic groupings of >900km are indicated by the three colors. Haplotypes represented by individuals from more than one geographic group were not colored.

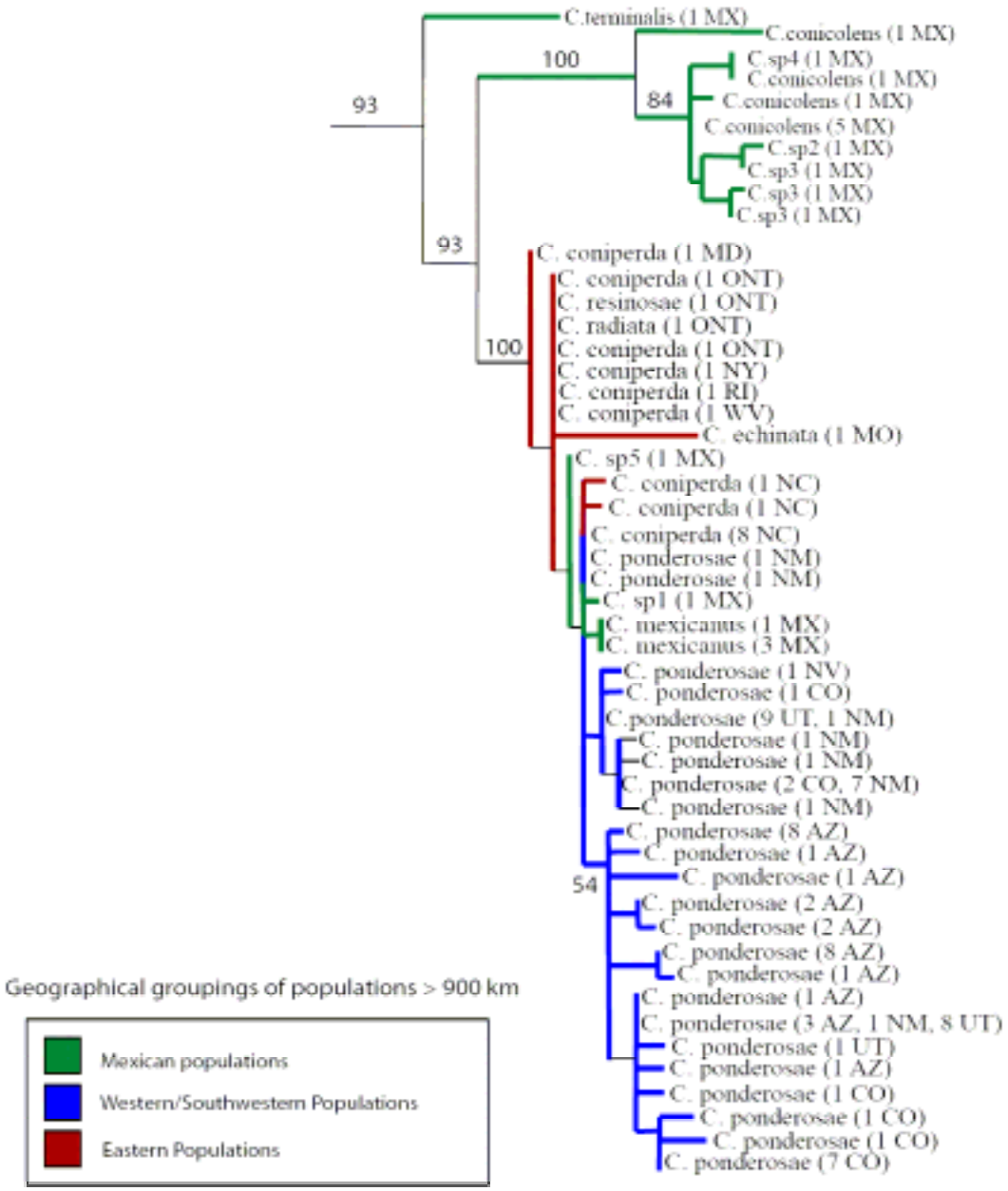

Figure 2.9. Geographic association of haplotypes of *Conophthorus* individuals sampled in major group two. Geographic groupings of >900km are indicated by the three colors. Haplotypes represented by individuals from more than one geographic group were not colored.

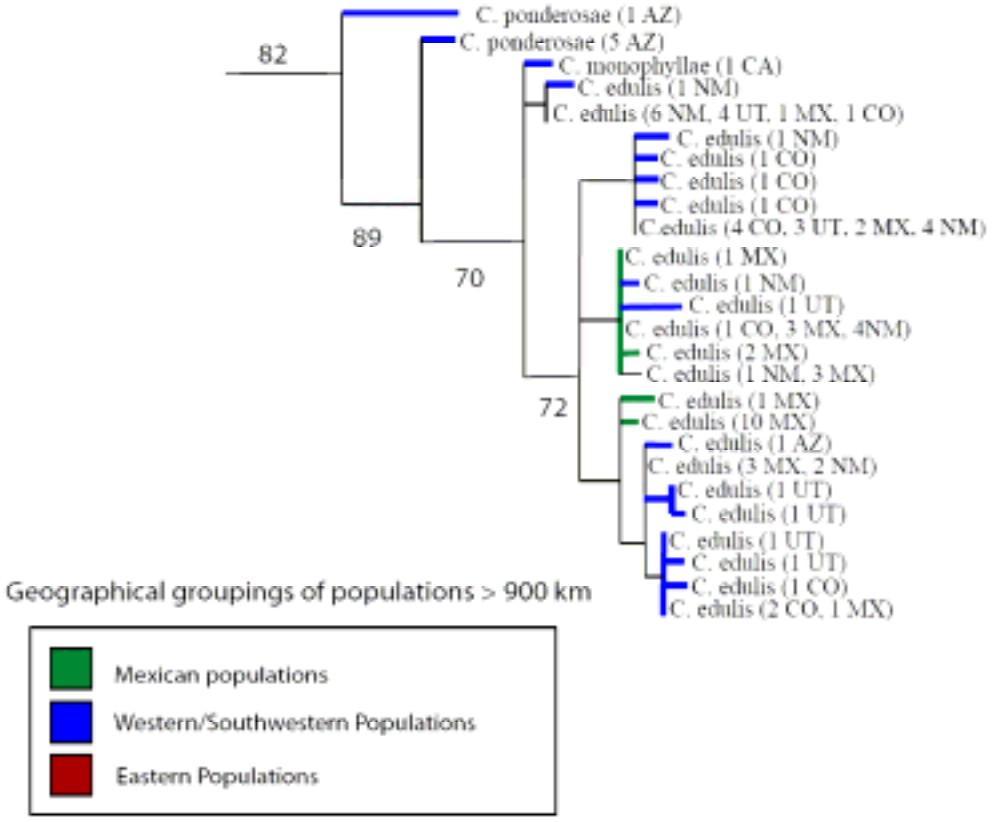

Figure 2.10. Geographic association of haplotypes of *Conophthorus* individuals sampled in major group three. Geographic groupings of >900km are indicated by the three colors. Haplotypes represented by individuals from more than one geographic group were not colored.

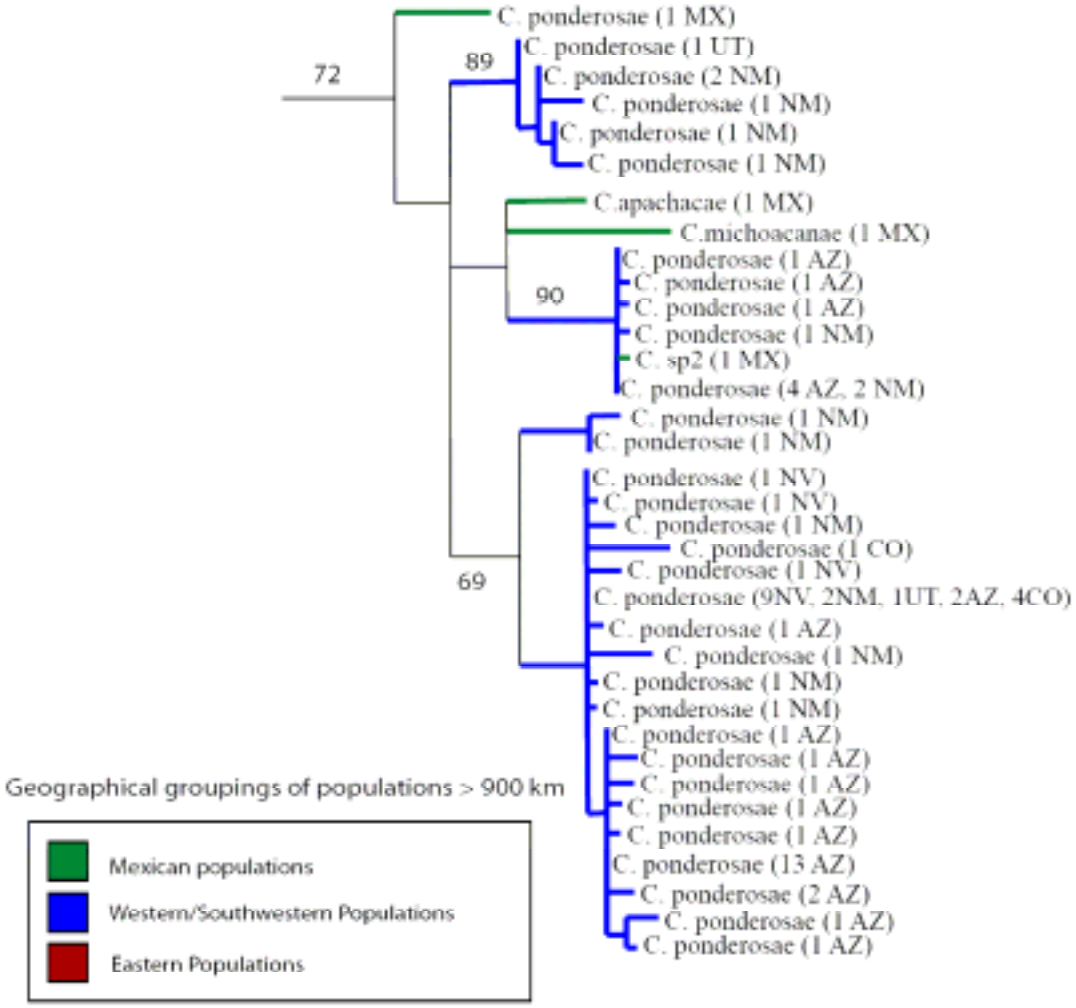

Figure 2.11. Geographic association of haplotypes of *Conophthorus* individuals sampled in major group four. Geographic groupings of >900km are indicated by the three colors. Haplotypes represented by individuals from more than one geographic group were not colored.

Haplotype Network of *Conophthorus edulis* based on 751bp of the mtDNA COI gene

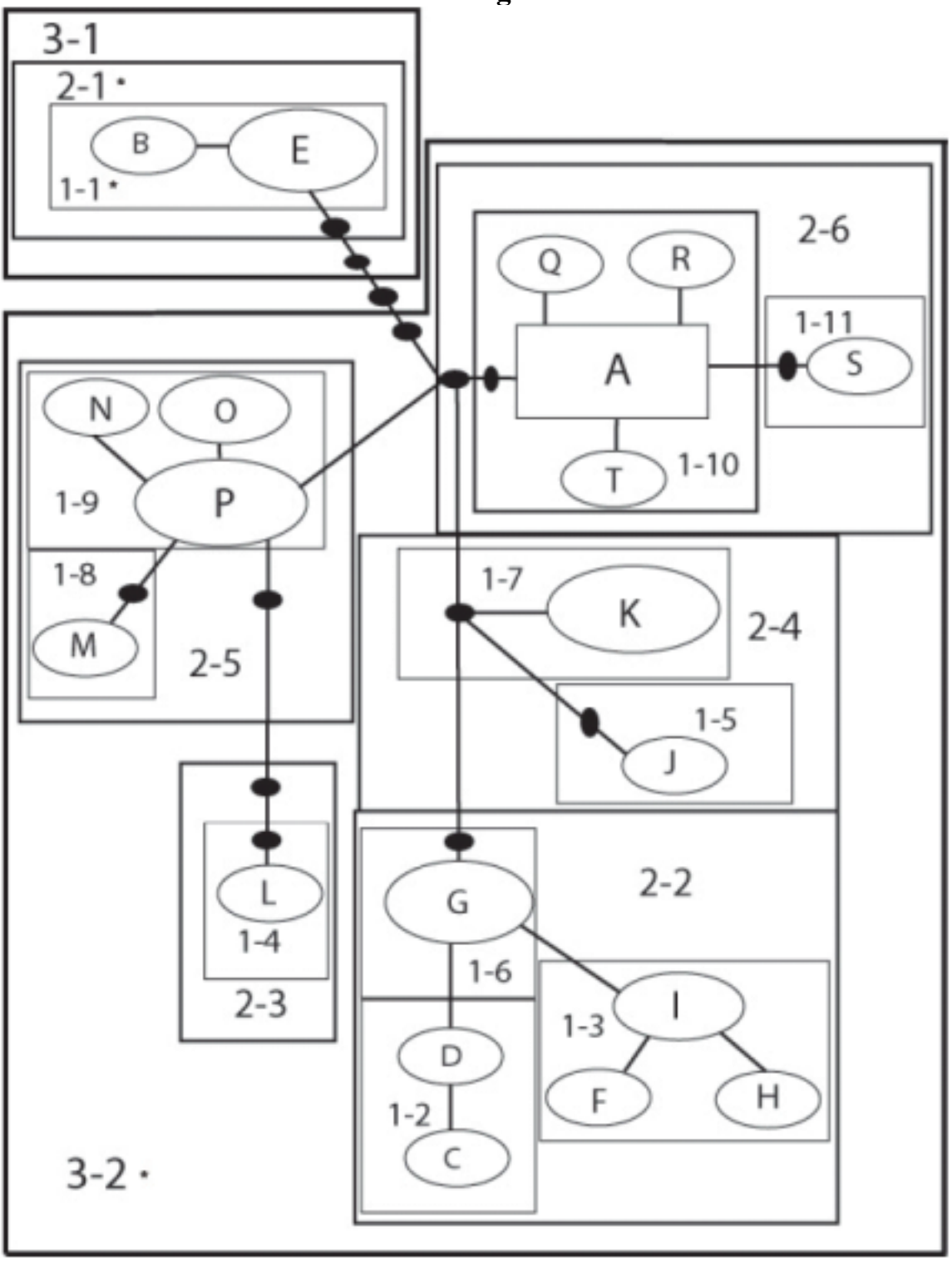

Figure 3.1. Haplotype network for *C.edulis*. Black ovals represent ancestral/missing haplotypes. The letters correspond to haplotypes designated in Table 2.3. Clades with * are significantly associated with geography.

Group 1 Haplotype Network of *Conophthorus ponderosae* based on 751bp of the mtDNA COI gene.

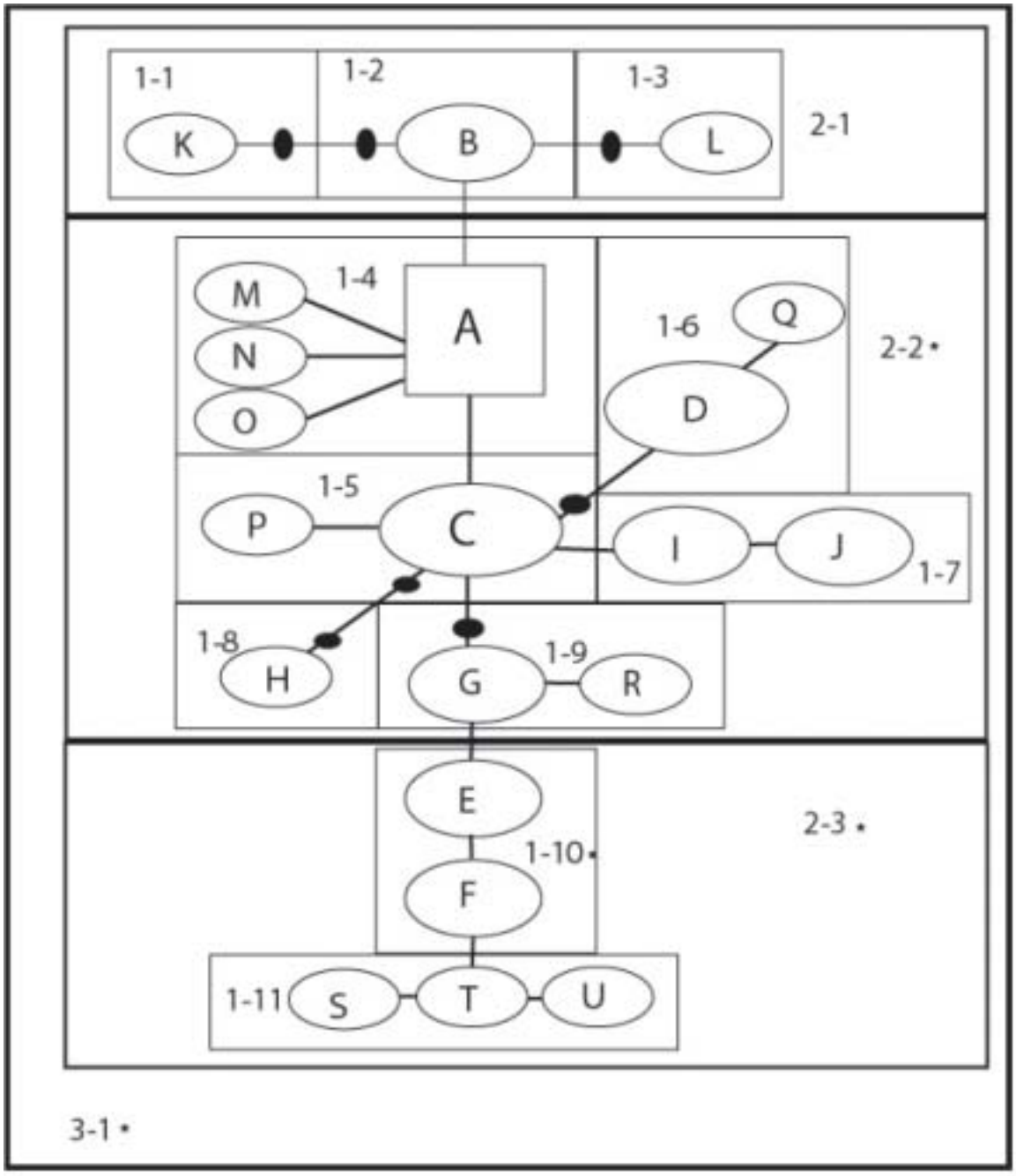

Figure 3.2 Group 1, first of three haplotype networks found for *C. ponderosae*. Letters correspond to haplotypes found in Table 2.4. Black ovals represent ancestral/missing haplotypes. Network includes individuals from the major clade two in Figure 2.1. Clades with * are significantly associated with geography.

Group 2 Haplotype Network of *Conophthorus ponderosae* based on 751bp of the mtDNA COI gene.

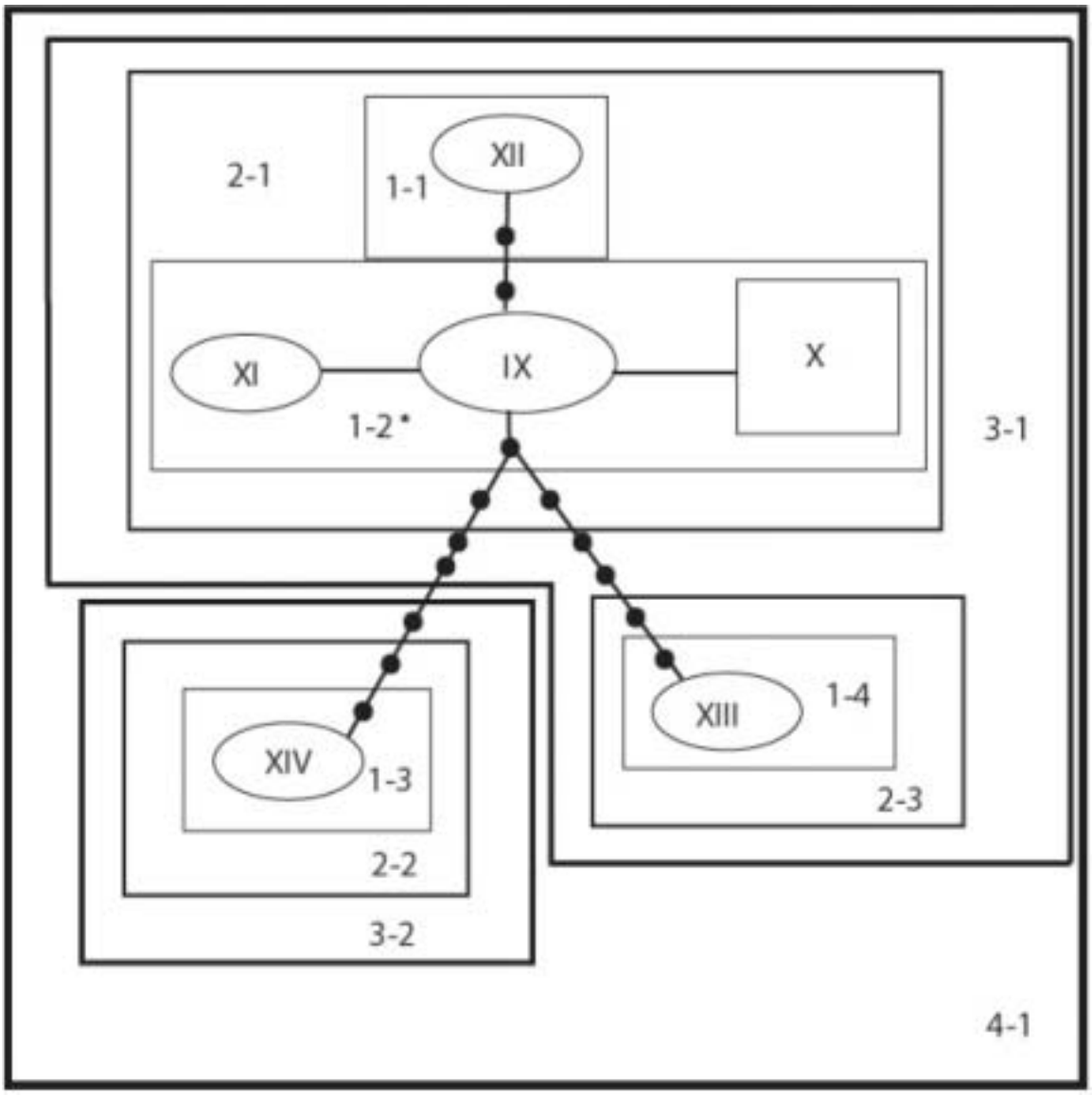

Figure 3.3. Group 2, second haplotype network of three found for *C. ponderosae*. Greek numbers correspond to haplotypes found in Table 2.5. Black ovals represent ancestral/missing haplotypes. Network includes individuals from the major clade one in Figure 2.1. Clades with * are significantly associated with geography.

Group 3 Haplotype Network of *Conophthorus ponderosae* based on 751bp of the mtDNA COI gene.

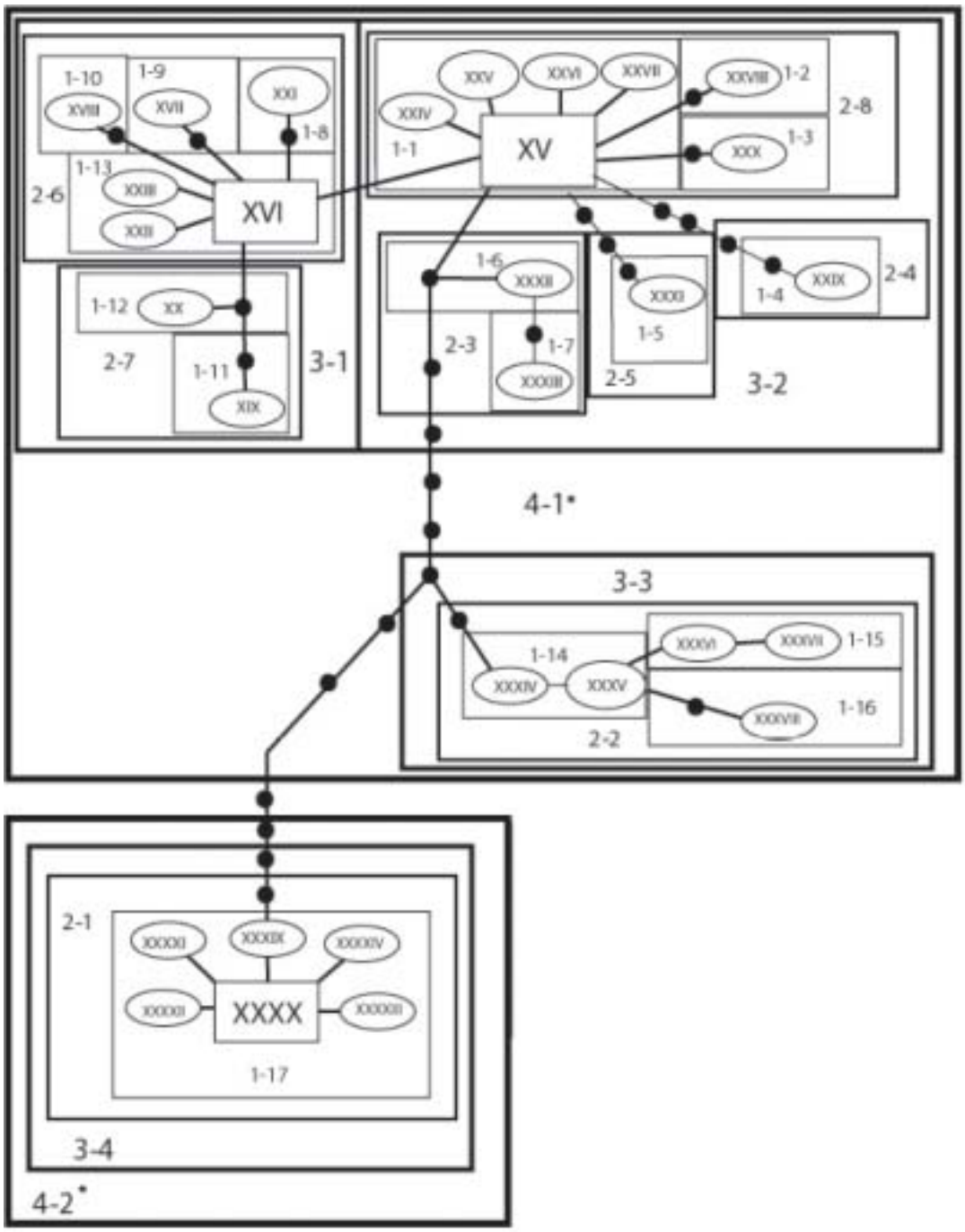

Figure 3.4. Group 3, third haplotype network of three found with *C. ponderosae*. Greek numbers correspond to haplotypes in Table 2.6. Black ovals represent ancestral/missing haplotypes. Network includes individuals from the major clade two and four of Figure 2.1. Clades with * are significantly associated with geography.

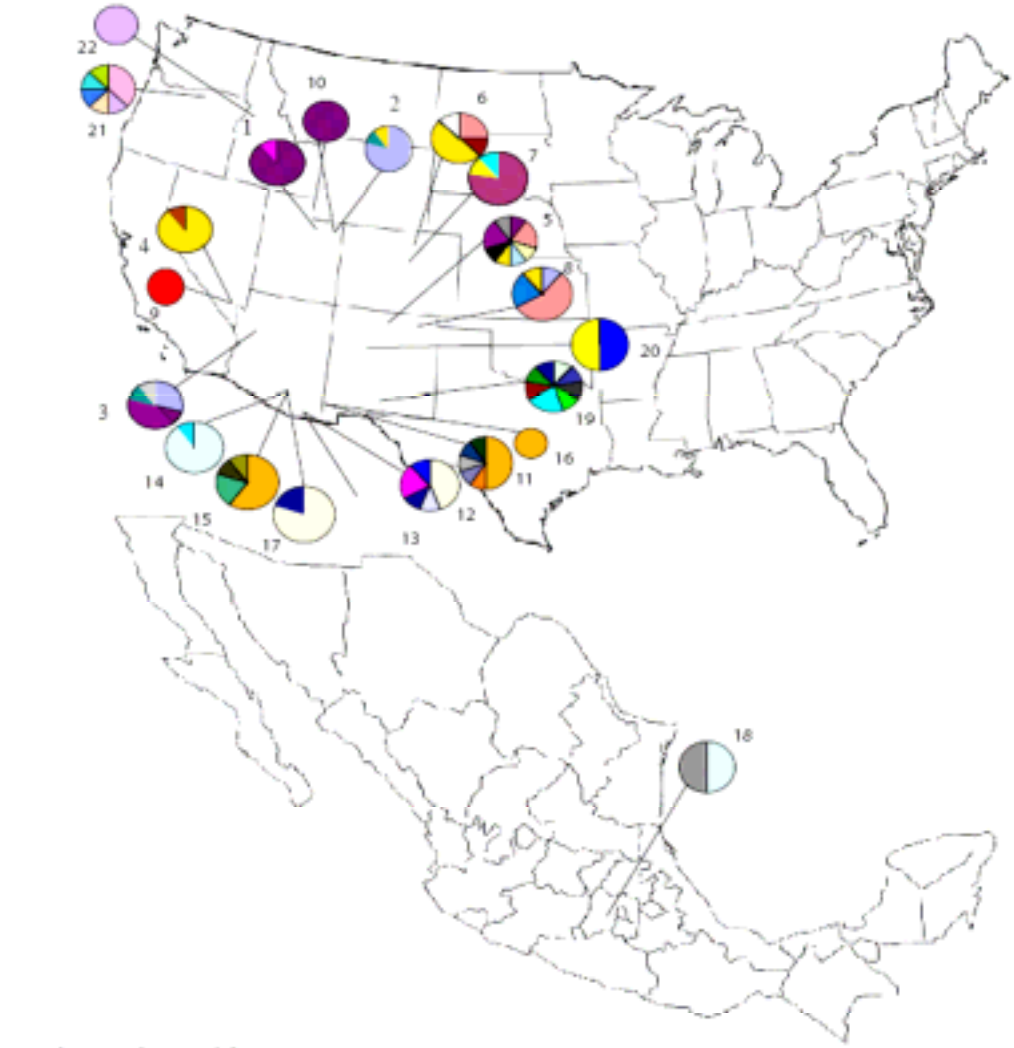

Figure 3.5.Geographic distribution of *C. ponderosae* haplotypes sampled in nested clade analysis. Numbers correspond to the localities, and colors to the haplotypes cited in the legends.

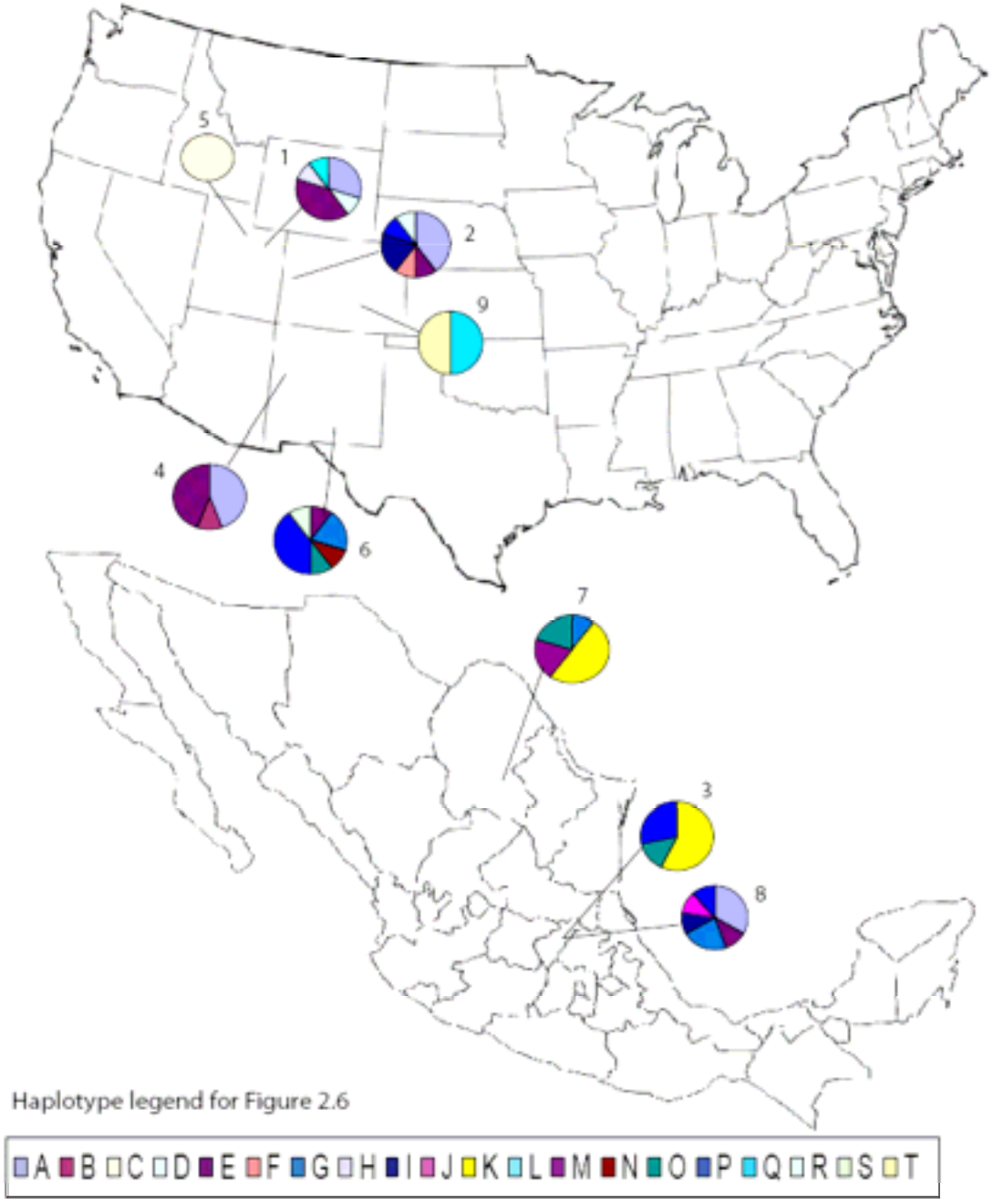

Figure 3.6.Geographic distribution of *C. edulis* haplotypes sampled in nested clade analysis. Numbers correspond to the localities, and patterns to the haplotypes cited in the legends

APPENDIX C

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
161	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
162	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
163	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
165	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
166	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
164	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
169	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
170	AD	Utah: Dagget Co. Ashley NF1	H	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
204	AD	New Mexico: Taos Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
308	AD	Utah: Dagget Co 2.	H	*C.ponderosae*	J	V	*P.flexilis*		*Strobus*	*Strobi*
202	AE	New Mexico: Taos Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
208	AF	New Mexico: Taos Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
203	AG	New Mexico: Taos Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
209	AG	New Mexico: Taos Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
275	AG	Colorado: Larimer Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
268	AG	Colorado: Larimer Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
289	AG	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
290	AG	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
291	AG	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
295	AG	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
296	AG	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
423	AH	New Mexico: Cibola Co.	H	*C.ponderosae*	E	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
233	SS	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
234	TT	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
231	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
232	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
235	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
236	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
237	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
238	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
239	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
240	UU	North Carolina: Cherokee Co.	H	*C. coniperda*	T	W	*P.strobus*		*Strobus*	*Strobi*
288	UU	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
293	UU	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
402	XX	Mexico: Mexico	H	*C.sp*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
408	ZZ	Mexico: Puebla	H	*C. mexicanus*	C	U	*P.patula*		*Pinus*	*Oocarpae*
409	ZZ	Mexico: Puebla	H	*C. mexicanus*	C	U	*P.patula*		*Pinus*	*Oocarpae*
410	ZZ	Mexico: Puebla	H	*C. mexicanus*	C	U	*P.patula*		*Pinus*	*Oocarpae*
331	AI	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
332	AI	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
336	AI	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
339	AI	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
375	AI	Arizona: Pima Co. 3 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
377	AI	Arizona: Pima Co. 3 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
378	AI	Arizona: Pima Co. 3 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
380	AI	Arizona: Pima Co. 3 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
337	AJ	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
338	AK	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
335	AL	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
379	AL	Arizona: Pima Co. 3 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
333	AM	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
334	AM	Arizona: Graham Co. 1 Pinaleno Mts.	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
351	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
352	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
353	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
354	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
355	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
356	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
358	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
360	AN	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
359	AO	Arizona: Pima Co. 1 St. Catalina Mts	H	*C.ponderosae*	D	V	*P.strobiformis*		*Strobus*	*Strobi*
171	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
172	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
173	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
174	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
175	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
176	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
177	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
178	AQ	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
182	AQ	Arizona: Coconino Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
188	AQ	Arizona: Coconino Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
189	AQ	Arizona: Coconino Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
292	AQ	New Mexico: Colfax Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
180	AR	Utah: Washington Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
185	AS	Arizona: Coconino Co.	H	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
271	AT	Colorado: Larimer Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
282	AU	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
284	AV	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
285	AW	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
277	AW	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
278	AW	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
279	AW	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
280	AW	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
281	AW	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
283	AW	Colorado: Saguache Co.	H	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
254	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
253	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
255	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
251	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
252	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
256	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
257	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
258	Z	Mexico	G	*C .conicolens*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
435	EE	Mexico: Mexico	G	*C.sp*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
436	FF	Mexico: Mexico	G	*C.sp*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
437	GG	Mexico: Mexico	G	*C.sp*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
438	HH	Mexico: Mexico	G	*C.sp*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
445	K	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
441	R	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
439	U	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
446	V	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
440	W	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
442	W	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
448	W	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
443	X	Oregon: Wasco Co.	E	*C.ponderosae*	P	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
449	X	Idaho: Idaho Co.	E	*C.ponderosae*	M	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
450	X	Idaho: Idaho Co.	E	*C.ponderosae*	M	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
451	X	Idaho: Idaho Co.	E	*C.ponderosae*	M	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
452	X	Idaho: Idaho Co.	E	*C.ponderosae*	M	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
453	X	Idaho: Idaho Co.	E	*C.ponderosae*	M	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
167	DF	Utah: Dagget Co. Ashley NF1	M	*C.ponderosae*	J	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
424	DG	New Mexico: Ortero Co.	M	*C.ponderosae*	E	V	*P.arizonica*		*Pinus*	*Ponderosae*
426	DG	New Mexico: Ortero Co.	M	*C.ponderosae*	E	V	*P.arizonica*		*Pinus*	*Ponderosae*
430	DH	New Mexico: Ortero Co.	M	*C.ponderosae*	E	V	*P.arizonica*		*Pinus*	*Ponderosae*
425	DI	New Mexico: Ortero Co.	M	*C.ponderosae*	E	V	*P.arizonica*		*Pinus*	*Ponderosae*
427	DJ	New Mexico: Ortero Co.	M	*C.ponderosae*	E	V	*P.arizonica*		*Pinus*	*Ponderosae*
361	EJ	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
181	DN	Arizona: Coconino Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
183	DO	Arizona: Coconino Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
205	DP	New Mexico: Taos Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
403	DQ	Mexico: Mexico	M	*C.sp*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
184	DR	Arizona: Coconino Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
186	DR	Arizona: Coconino Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
187	DR	Arizona: Coconino Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
190	DR	Arizona: Coconino Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
206	DR	New Mexico: Taos Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
210	DR	New Mexico: Taos Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
431	DS	New Mexico: Cibola Co.	M	*C.ponderosae*	E	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
432	DT	New Mexico: Cibola Co.	M	*C.ponderosae*	E	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
199	DV	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
207	DW	New Mexico: Taos Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
273	DX	Colorado: Larimer Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
307	DY	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.flexilis*	*brachyptera*	*Strobus*	*Strobi*
191	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
192	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
193	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
194	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
195	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
196	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
197	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
198	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
200	DZ	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
179	DZ	Utah: Washington Co.	M	*C.ponderosae*	F	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
201	DZ	New Mexico: Taos Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
274	DZ	Colorado: Larimer Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
276	DZ	Colorado: Larimer Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
269	DZ	Colorado: Larimer Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
270	DZ	Colorado: Larimer Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*scopulorum*	*Pinus*	*Ponderosae*
287	DZ	New Mexico: Colfax Co.	M	*C.ponderosae*	I	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
342	DZ	Arizona: Graham Co. 2 Pinaleno Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
343	DZ	Arizona: Graham Co. 2 Pinaleno Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
350	EF	Arizona: Graham Co. 2 Pinaleno Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
422	EG	New Mexico: Cibola Co.	M	*C.ponderosae*	E	V	*P.ponderosa*	*brachyptera*	*Pinus*	*Ponderosae*
428	EH	New Mexico: Ortero Co.	M	*C.ponderosae*	E	V	*P.arizonica*		*Pinus*	*Ponderosae*
429	EI	New Mexico: Ortero Co.	M	*C.ponderosae*	E	V	*P.arizonica*		*Pinus*	*Ponderosae*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
323	EK	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
324	EL	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
329	EM	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
368	EN	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
321	EO	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
322	EO	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
326	EO	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
327	EO	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
328	EO	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
362	EO	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
365	EO	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
366	EO	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
367	EO	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
369	EO	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
370	EO	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
371	EO	Arizona: Conchise Co. 2 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.leiophylla*		*Pinus*	*Leiophyllae*
374	EO	Arizona: Conchise Co. 2 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.leiophylla*		*Pinus*	*Leiophyllae*
325	EQ	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
330	ER	Arizona: Conchise Co. 1 Chiricahua Mts.	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
363	EP	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
364	EP	Arizona: Pima Co. 2 St. Catalina Mts	M	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
349	AX	Arizona: Graham Co. 2 Pinaleno Mts.	J	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
341	AY	Arizona: Graham Co. 2 Pinaleno Mts.	J	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
344	AY	Arizona: Graham Co. 2 Pinaleno Mts.	J	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
345	AY	Arizona: Graham Co. 2 Pinaleno Mts.	J	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
346	AY	Arizona: Graham Co. 2 Pinaleno Mts.	J	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
348	AY	Arizona: Graham Co. 2 Pinaleno Mts.	J	*C.ponderosae*	D	V	*P.arizonica*		*Pinus*	*Ponderosae*
393	BC	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
218	BD	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
243	BD	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
244	BD	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
249	BD	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
250	BD	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
313	BD	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
387	BD	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
395	BD	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
396	BD	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
397	BD	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
400	BD	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
217	BK	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
245	BL	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
214	BM	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
215	BM	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
216	BM	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
219	BM	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
263	BM	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
266	BM	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
314	BM	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
389	BM	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
223	BN	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
227	BN	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
211	BO	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
221	BO	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
222	BO	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
261	BO	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
220	BE	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
299	BF	Colorado: Chaffee Co.	K	*C. edulis*	I	V	*P.edulis*		*Strobus*	*Cembroides*
303	BG	Colorado: Chaffee Co.	K	*C. edulis*	I	V	*P.edulis*		*Strobus*	*Cembroides*
312	BH	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
241	BI	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
246	BI	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
247	BI	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
316	BI	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
317	BI	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
318	BI	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
320	BI	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
382	BI	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
383	BI	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
390	BI	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
391	BI	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
392	BI	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
394	BI	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
399	BI	New Mexico: Cibola Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
388	BQ	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
224	BR	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
225	BR	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
226	BR	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
228	BR	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
229	BR	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
259	BR	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
260	BR	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
262	BR	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
265	BR	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
407	BR	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
212	BT	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
213	BT	New Mexico: Ortero Co.	K	*C. edulis*	E	V	*P.edulis*		*Strobus*	*Cembroides*
230	BT	Mexico: Coahuila	K	*C. edulis*	B	U	*P.cembroides*		*Strobus*	*Cembroides*
385	BT	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
386	BT	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
242	BU	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
420	BV	Utah: Duchesne Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
248	BX	Utah: Grand Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
311	BY	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
315	BZ	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
319	BZ	Colorado: Dolores Co.	K	*C. edulis*	J	V	*P.edulis*		*Strobus*	*Cembroides*
381	BZ	Mexico: Queretaro.	K	*C. edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
105.coli	A	MEX: Michoacan	A	*C.conicolens*	C	U	*P.pseudostrobus*		*Pinus*	*Ponderosae*
35.teco	B	MEX: Michoacan	B	*C.teocotum*	C	U	*P.teocote*		*Pinus*	*Ponderosae*
105.lam2C	C	USA:CA: Riverside Co.	C	*C.ponderosae*	G	V	*P.lamberitana*		*Strobus*	*Strobi*
MC9lam.b	D	MEX: Baja California	C	*C.ponderosae*	H	V	*P.lamberitana*		*Strobus*	*Strobi*
110.radj	E	USA:CA: Alameda Co.	D	*C.radiatae*	K	V	*P.radiata*		*Pinus*	*Oocarpae*
31.pond.C	F	USA:CA: Calaveras Co.	E	*C.ponderosae*	K	V	*P.ponderosa*	*benthamiana*	*Pinus*	*Ponderosae*
112.pon3C	G	USA:CA: Siskiyou Co.	E	*C.ponderosae*	L	V	*P.ponderosa*	*benthamiana*	*Pinus*	*Ponderosae*
40.lambCA	H	USA:CA: El Dorado Co. 1	E	*C.ponderosae*	K	V	*P.lamberitana*		*Strobus*	*Strobi*
111.lamb4	I	USA:CA: El Dorado Co. 2	E	*C.ponderosae*	K	V	*P.lamberitana*		*Strobus*	*Strobi*
127.lam6.(	J	USA:CA: Fresno Co.	E	*C.ponderosae*	K	V	*P.lamberitana*		*Strobus*	*Strobi*
121.lam5.(	L	USA:CA: Mendicino Co.	E	*C.ponderosae*	K	V	*P.lamberitana*		*Strobus*	*Strobi*
129.pon5.(	M	USA:CA: Riverside Co.	E	*C.ponderosae*	G	V	*P.ponderosa*	*benthamiana*	*Pinus*	*Ponderosae*
130.pon6.(	N	USA:CA: San Bernardino Co.	E	*C.ponderosae*	G	V	*P.ponderosa*	*benthamiana*	*Pinus*	*Ponderosae*
123.mont.	O	CAN: British Columbia	E	*C.ponderosae*	O	V	*P.monticola*		*Strobus*	*Strobi*
118.cont.E	P	CAN:British Columbia	E	*C.ponderosae*	N	V	*P.contorta*		*Pinus*	*Contortae*
119.con2.(	Q	CAN:British Columbia	E	*C.ponderosae*	N	V	*P.monticola*		*Strobus*	*Strobi*
117.pon2 (	S	USA:ID: Bonner Co.	E	*C.ponderosae*	M	V	*P.ponderosa*	*ponderosa*	*Pinus*	*Ponderosae*
101.mont	T	USA:ID: Kootenai Co.	E	*C.ponderosae*	M	V	*P.monticola*		*Strobus*	*Strobi*
122.term	Y	Mexico: Nuevo Leon	F	*C.terminales*	B	U	*not recorded*			
MC2.leph	AA	MEX:Mexico	G	*C.sp4*	C	U	*P.leiophylla*		*Pinus*	*Leiophyllae*
124.con2.(	II	Maryland: Anne Arundal Co.	H	*C. coniperda*	P	V	*P.strobus*		*Strobus*	*Strobi*
41.bank	JJ	CAN: Ontario	H	*C.radiatae*	R	W	*P.banksiana*		*Pinus*	*Contortae*
48.resi	KK	CAN: Ontario	H	*C.resinosae*	R	W	*P.resinosa*		*Pinus*	*Sylvestres*
52.cono	LL	CAN:Ontario	H	*C.coniperda*	R	W	*P.strobus*		*Strobus*	*Strobi*
85.con1	MM	CAN:Ontario	H	*C.coniperda*	R	W	*P.strobus*		*Strobus*	*Strobi*
125.con3N	NN	New York: Suffolk Co.	H	*C.coniperda*	Q	W	*P.strobus*		*Strobus*	*Strobi*
126.con4R	OO	Rhode Island: Lincoln Co.	H	*C.coniperda*	Q	W	*P.strobus*		*Strobus*	*Strobi*
132.cono.(	PP	West Virginia: Pendleton Co.	H	*C.coniperda*	P	V	*P.rigida*		*Pinus*	*Australes*

Cono hap code	Hap letter	Locality	ESC	Species	200-300km	>900km	Host	Subspecies	Subgenera	Section
141.ech1	QQ	USA:MO: Carter Co.	I	*C.echinata*	S	W	*P.echinata*		*Pinus*	*Australes*
MC3.mon2	RR	MEX:Mexico	H	*C.sp5*	C	U	*P.montezumae*		*Pinus*	*Ponderosae*
MC1.mexi	YY	MEX: Hidalgo	H	*C.mexicanus*	C	U	*P.patula*		*Pinus*	*Oocarpae*
109.flex.N	AB	USA:NV: White Pine Co.	H	*C.ponderosae*	F	V	*P.flexilis*		*Strobus*	*Strobi*
128.arist.C	AC	USA:CO: Park Co.	H	*C.ponderosae*	F	V	*P.aristata*		*Strobus*	*Balfouriana*
110.pon4.A	AP	USA:AZ: Coconino Co.	H	*C.ponderosae*	F	V	*P.arizonica*		*Pinus*	*Ponderosae*
37.mono	AZ	USA:CA: Riverside Co.	K	*C.monophyllae*	G	V	*P.monophylla*		*Strobus*	*Cembroides*
MC5.cem2	BJ	MEX: Hidalgo	K	*C.edulis*	C	U	*P.cembroides*		*Strobus*	*Cembroides*
39.cemb	BS	USA:AZ: Cochise Co.	K	*C.edulis*	D	V	*P.cembroides*		*Strobus*	*Cembroides*
108.edu1	BW	USA:UT: Kane Co.	K	*C.edulis*	F	V	*P.edulis*		*Strobus*	*Cembroides*
MC4.hart	DE	Mexico: Mexico	M	*C.ponderosae*	C	U	*P.hartwegii*		*Pinus*	*Ponderosae*
MC8.enge	DK	Mexico: Durango	M	*C.apachecae*	A	U	*P.engelmanni*		*Pinus*	*Ponderosae*
107.mich	DL	Mexico: Michoacan	L	*C.michoacanae*	C	U	*P.michoacana*		*Pinus*	*Ponderosae*
MC10.ariz	DM	Mexico: Durango	M	*C.ponderosae*	A	U	*P.arizonica*		*Pinus*	*Ponderosae*
115.fle2.N	DU	Nevada: Clark Co.	M	*C.ponderosae*	F	V	*P.flexilis*		*Strobus*	*Strobi*

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